



Corrected Sequence Listing2.ST25
SEQUENCE LISTING

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<110> Poustka, et al.

<120> PROTEIN (TP) THAT IS INVOLVED IN THE DEVELOPMENT OF THE NERVOUS SYSTEM

<130> 4121-129

<140> 09/914,549

<141> 2001-08-24

<150> PCT/DE00/00583

<151> 2000-02-28

<150> DE 199 08 423.8

<151> 1999-02-26

<160> 39

<170> PatentIn version 3.1

<210> 1

<211> 242

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (3)..(242)

<223>

<400> 1

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Arg Val Thr His Ala Ser Pro Pro Ser Glu Ala Ser Gln Ala Lys
1 5 10 15

acc cag caa gat atg cag tcc agt ctg gca gcc aga tat gca act cag 95
Thr Gln Gln Asp Met Gln Ser Ser Leu Ala Ala Arg Tyr Ala Thr Gln
20 25 30

tct aat cac agt gga att gca acc agt caa aaa aag cct act agg ctt 143
Ser Asn His Ser Gly Ile Ala Thr Ser Gln Lys Lys Pro Thr Arg Leu
35 40 45

cca ggg ccc tct agg gtg cct gct gca gga agc agc agc aag gtc cag 191
Pro Gly Pro Ser Arg Val Pro Ala Ala Gly Ser Ser Lys Val Gln
50 55 60

gga gcc tct aat tta aat agg aga agt cag agc ttt aac agc att gac 239
Gly Ala Ser Asn Leu Asn Arg Arg Ser Gln Ser Phe Asn Ser Ile Asp
65 70 75

aaa 242
Lys
80

<210> 2

<211> 80

<212> PRT

<213> Homo sapiens

<400> 2

Corrected Sequence Listing2.ST25

Arg Val Thr His Ala Ser Pro Pro Ser Glu Ala Ser Gln Ala Lys Thr
1 5 10 15

Gln Gln Asp Met Gln Ser Ser Leu Ala Ala Arg Tyr Ala Thr Gln Ser
20 25 30

Asn His Ser Gly Ile Ala Thr Ser Gln Lys Lys Pro Thr Arg Leu Pro
35 40 45

Gly Pro Ser Arg Val Pro Ala Ala Gly Ser Ser Ser Lys Val Gln Gly
50 55 60

Ala Ser Asn Leu Asn Arg Arg Ser Gln Ser Phe Asn Ser Ile Asp Lys
65 70 75 80

<210> 3
<211> 159
<212> DNA
<213> Homo sapiens

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<221> CDS
<222> (1)..(159)
<223>

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Gly Thr His Glu Val Gln Ser Leu Leu Met Arg Thr Gly Ser Val Arg
1 5 10 15

tct act ctc tca gaa aga tat acc cca tca tct cgg cag gcc aac caa 96
Ser Thr Leu Ser Glu Arg Tyr Thr Pro Ser Ser Arg Gln Ala Asn Gln
20 25 30

gaa gag ggc aaa gag tgg ttg cgt tct cat tct act gga ggg ctt cag 144
Glu Glu Gly Lys Glu Trp Leu Arg Ser His Ser Thr Gly Gly Leu Gln
35 40 45

gac act ggc aac cag 159
Asp Thr Gly Asn Gln
50

<210> 4
<211> 53
<212> PRT
<213> Homo sapiens

<400> 4
Gly Thr His Glu Val Gln Ser Leu Leu Met Arg Thr Gly Ser Val Arg
1 5 10 15

Ser Thr Leu Ser Glu Arg Tyr Thr Pro Ser Ser Arg Gln Ala Asn Gln
20 25 30

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Glu Glu Gly Lys Glu Trp Leu Arg Ser His Ser Thr Gly Gly Leu Gln
35 40 45

Asp Thr Gly Asn Gln
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<210> 5
<211> 2461
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (2)..(1627)
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1 5 10 15
ctg aaa gca gag aat gac cga ctg aag gta gcc cca ggc ccc tca tca 97
Leu Lys Ala Glu Asn Asp Arg Leu Lys Val Ala Pro Gly Pro Ser Ser
20 25 30
ggc tcc act cca ggg cag gtc cct gga tca tct gca tta tct tcc cca 145
Gly Ser Thr Pro Gly Gln Val Pro Gly Ser Ser Ala Leu Ser Ser Pro
35 40 45
cgc cgc tcc cta ggc ctg gca ctc acc cat tcc ttc ggc ccc agt ctt 193
Arg Arg Ser Leu Gly Leu Ala Leu Thr His Ser Phe Gly Pro Ser Leu
50 55 60
gca gac aca gac ctg tca ccc atg gat ggc atc agt act tgt ggt cca 241
Ala Asp Thr Asp Leu Ser Pro Met Asp Gly Ile Ser Thr Cys Gly Pro
65 70 75 80
aag gag gaa gtg acc ctc cgg gtg gtg gtg agg atg ccc ccg cag cac 289
Lys Glu Glu Val Thr Leu Arg Val Val Val Arg Met Pro Pro Gln His
85 90 95
atc atc aaa ggg gac ttg aag cag cag gaa ttc ttc ctg ggc tgt agc 337
Ile Ile Lys Gly Asp Leu Lys Gln Gln Glu Phe Phe Leu Gly Cys Ser
100 105 110
aag gtc agt gga aaa gtt gac tgg aag atg ctg gat gaa gct gtt ttc 385
Lys Val Ser Gly Lys Val Asp Trp Lys Met Leu Asp Glu Ala Val Phe
115 120 125
caa gtg ttc aag gac tat att tct aaa atg gac cca gcc tct acc ctg 433
Gln Val Phe Lys Asp Tyr Ile Ser Lys Met Asp Pro Ala Ser Thr Leu
130 135 140
gga cta agc act gag tcc atc cat ggc tac agc atc agc cac gtg aaa 481
Gly Leu Ser Thr Glu Ser Ile His Gly Tyr Ser Ile Ser His Val Lys
145 150 155 160
cga gtg ttg gat gca gag ccc ccc gag atg cct cct tgc cgt cga ggt 529
Arg Val Leu Asp Ala Glu Pro Pro Glu Met Pro Pro Cys Arg Arg Gly
165 170 175

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gtc aat aac ata tca gtc tcc ctc aaa ggt ctg aag gag aaa tgc gtc Val Asn Asn Ile Ser Val Ser Leu Lys Gly Leu Lys Glu Lys Cys Val 180 185 190	577
gac agc ctg gtg ttc gag acg ctg atc ccc aag ccg atg atg cag cac Asp Ser Leu Val Phe Glu Thr Leu Ile Pro Lys Pro Met Met Gln His 195 200 205	625
tac ata agc ctc ctg ctg aag cac cgg cgc ctc gtc ctc tcg ggc ccc Tyr Ile Ser Leu Leu Leu Lys His Arg Arg Leu Val Leu Ser Gly Pro 210 215 220	673
agc ggc acg ggc aag acc tac ctg acc aat cgc ttg gcc gag tac ctg Ser Gly Thr Gly Lys Thr Tyr Leu Thr Asn Arg Leu Ala Glu Tyr Leu 225 230 235 240	721
gtg gag cgc tct ggc cgt gag gtc aca gag ggc atc gtc agc acc ttc Val Glu Arg Ser Gly Arg Glu Val Thr Glu Gly Ile Val Ser Thr Phe 245 250 255	769
aac atg cac cag cag tct tgc aag gat ctg caa ctg tat ctt tcc aac Asn Met His Gln Gln Ser Cys Lys Asp Leu Gln Leu Tyr Leu Ser Asn 260 265 270	817
cta gcc aac cag ata gac cgg gaa aca gga att ggg gat gtg ccc ctg Leu Ala Asn Gln Ile Asp Arg Glu Thr Gly Ile Gly Asp Val Pro Leu 275 280 285	865
gtg att cta ttg gat gac ctg agt gaa gca ggc tcc atc agt gag ttg Val Ile Leu Leu Asp Asp Leu Ser Glu Ala Gly Ser Ile Ser Glu Leu 290 295 300	913
gtc aat ggg gcc ctc acc tgc aag tat cat aaa tgt ccc tat att ata Val Asn Gly Ala Leu Thr Cys Lys Tyr His Lys Cys Pro Tyr Ile Ile 305 310 315 320	961
ggt acc acc aat cag cct gta aaa atg aca ccc aac cat ggc ttg cac Gly Thr Thr Asn Gln Pro Val Lys Met Thr Pro Asn His Gly Leu His 325 330 335	1009
ttg agc ttc agg atg ttg acc ttc tcc aac aac gtg gag cca gcc aat Leu Ser Phe Arg Met Leu Thr Phe Ser Asn Asn Val Glu Pro Ala Asn 340 345 350	1057
ggc ttc ctg gtt cgt tac ctg agg agg aag ctg gta gag tca gac agc Gly Phe Leu Val Arg Tyr Leu Arg Arg Lys Leu Val Glu Ser Asp Ser 355 360 365	1105
gac atc aat gcc aac aag gaa gag ctg ctt cgg gtg ctc gac tgg gta Asp Ile Asn Ala Asn Lys Glu Glu Leu Leu Arg Val Leu Asp Trp Val 370 375 380	1153
ccc aag ctg tgg tat cat ctc cac acc ttc ctt gag aag cac agc acc Pro Lys Leu Trp Tyr His Leu His Thr Phe Leu Glu Lys His Ser Thr 385 390 400	1201
tca gac ttc ctc atc ggc cct tgc ttc ttt ctg tcg tgt ccc att ggc Ser Asp Phe Leu Ile Gly Pro Cys Phe Phe Leu Ser Cys Pro Ile Gly 405 410 415	1249
att gag gac ttc cgg acc tgg ttc att gac ctg tgg aac aac tct atc Ile Glu Asp Phe Arg Thr Trp Phe Ile Asp Leu Trp Asn Asn Ser Ile 420 425 430	1297

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420	425	430	
att ccc tat cta cag gaa gga gcc aag gat ggg ata aag gtc cat gga Ile Pro Tyr Leu Gln Glu Gly Ala Lys Asp Gly Ile Lys Val His Gly 435 440 445			1345
cag aaa gct gct tgg gag gac cca gtg gaa tgg gtc cgg gac aca ctt Gln Lys Ala Ala Trp Glu Asp Pro Val Glu Trp Val Arg Asp Thr Leu 450 455 460			1393
ccc tgg cca tca gcc caa caa gac caa tca aag ctg tac cac ctg ccc Pro Trp Pro Ser Ala Gln Gln Asp Gln Ser Lys Leu Tyr His Leu Pro 465 470 475 480			1441
cca ccc acc gtg ggc cct cac agc att gcc tca cct ccc gag gat agg Pro Pro Thr Val Gly Pro His Ser Ile Ala Ser Pro Pro Glu Asp Arg 485 490 495			1489
aca gtc aaa gac agc acc cca agt tct ctg gac tca gat cct ctg atg Thr Val Lys Asp Ser Thr Pro Ser Ser Leu Asp Ser Asp Pro Leu Met 500 505 510			1537
gcc atg ctg ctg aaa ctt caa gaa gct gcc aac tac att gag tct cca Ala Met Leu Leu Lys Leu Gln Glu Ala Ala Asn Tyr Ile Glu Ser Pro 515 520 525			1585
gat cga gaa acc atc ctg gac ccc aac ctt cag gca aca ctt Asp Arg Glu Thr Ile Leu Asp Pro Asn Leu Gln Ala Thr Leu 530 535 540			1627
taagggttcg gcaatcactg tcacccccgg acagcagaac gctggcatca gctatcttag			1687
ctcctcctct cccctctcct ctttcagagc actggctctc cagccccagg aggagaacag			1747
gagggaggag gagatgaaag aggagggaca ggttcttggt gctgtacctt tgagaacttc			1807
ctaggaagga atggtggggg ggcgtttggg aacttggtgcc ccctaaacac atttactggc			1867
ctcctctaatt gactttgggg aaaagatgat tctgggtctt tcccttgact tcttgtttca			1927
attacaaact cctgggcttt ctggggaggg gttcagaaaa catcaaaaaca ctgcagcagt			1987
tcctaaatga ttctcacaag caaccctgag agagacagtc ttgtgagggg gatctggggg			2047
aggcaggaag ctctcagat ttctcacag acccttccca attccatcac cactgccaac			2107
aactcctccc ccagagatct ggctggagcc cagaaaaaga agcatgtggt ttaaaaaatg			2167
tttaaatcaa tctgtaaaag gtaaaaatga aaaacaaaaa caagcaaaca aacaaaaaac			2227
aatggaaaag atgaagctgg agagagagga accagttgcc aaggtagaga gctgcccgt			2287
cctgccctct ggatgacata ggggacatca acaagacggc tgccaacctg agaagtcacc			2347
aaaccacaaa aataacctta cagccttcag ggaaagacta ccagctctgt ctttctaccc			2407
tctaatttaa caatgcataa gagtcaataa accctacttt tttaaaaaaa aaaa			2461

<210> 6
 <211> 542
 <212> PRT
 <213> Homo sapiens

Corrected Sequence Listing2.ST25

<400> 6

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Asp Gln Leu Arg Glu Thr Met His Asn Met Gln Leu Glu Val Asp Leu
1      5      10      15
Leu Lys Ala Glu Asn Asp Arg Leu Lys Val Ala Pro Gly Pro Ser Ser
20      25      30
Gly Ser Thr Pro Gly Gln Val Pro Gly Ser Ser Ala Leu Ser Ser Pro
35      40      45
Arg Arg Ser Leu Gly Leu Ala Leu Thr His Ser Phe Gly Pro Ser Leu
50      55      60
Ala Asp Thr Asp Leu Ser Pro Met Asp Gly Ile Ser Thr Cys Gly Pro
65      70      75      80
Lys Glu Glu Val Thr Leu Arg Val Val Val Arg Met Pro Pro Gln His
85      90      95
Ile Ile Lys Gly Asp Leu Lys Gln Gln Glu Phe Phe Leu Gly Cys Ser
100     105     110
Lys Val Ser Gly Lys Val Asp Trp Lys Met Leu Asp Glu Ala Val Phe
115     120     125
Gln Val Phe Lys Asp Tyr Ile Ser Lys Met Asp Pro Ala Ser Thr Leu
130     135     140
Gly Leu Ser Thr Glu Ser Ile His Gly Tyr Ser Ile Ser His Val Lys
145     150     155     160
Arg Val Leu Asp Ala Glu Pro Pro Glu Met Pro Pro Cys Arg Arg Gly
165     170     175
Val Asn Asn Ile Ser Val Ser Leu Lys Gly Leu Lys Glu Lys Cys Val
180     185     190
Asp Ser Leu Val Phe Glu Thr Leu Ile Pro Lys Pro Met Met Gln His
195     200     205
Tyr Ile Ser Leu Leu Leu Lys His Arg Arg Leu Val Leu Ser Gly Pro
210     215     220
Ser Gly Thr Gly Lys Thr Tyr Leu Thr Asn Arg Leu Ala Glu Tyr Leu
225     230     235     240

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Corrected Sequence Listing2.ST25

Val Glu Arg Ser Gly Arg Glu Val Thr Glu Gly Ile Val Ser Thr Phe
 245 250 255
 Asn Met His Gln Gln Ser Cys Lys Asp Leu Gln Leu Tyr Leu Ser Asn
 260 265 270
 Leu Ala Asn Gln Ile Asp Arg Glu Thr Gly Ile Gly Asp Val Pro Leu
 275 280 285
 Val Ile Leu Leu Asp Asp Leu Ser Glu Ala Gly Ser Ile Ser Glu Leu
 290 295 300
 Val Asn Gly Ala Leu Thr Cys Lys Tyr His Lys Cys Pro Tyr Ile Ile
 305 310 315 320
 Gly Thr Thr Asn Gln Pro Val Lys Met Thr Pro Asn His Gly Leu His
 325 330 335
 Leu Ser Phe Arg Met Leu Thr Phe Ser Asn Asn Val Glu Pro Ala Asn
 340 345 350
 Gly Phe Leu Val Arg Tyr Leu Arg Arg Lys Leu Val Glu Ser Asp Ser
 355 360 365
 Asp Ile Asn Ala Asn Lys Glu Glu Leu Leu Arg Val Leu Asp Trp Val
 370 375 380
 Pro Lys Leu Trp Tyr His Leu His Thr Phe Leu Glu Lys His Ser Thr
 385 390 395 400
 Ser Asp Phe Leu Ile Gly Pro Cys Phe Phe Leu Ser Cys Pro Ile Gly
 405 410 415
 Ile Glu Asp Phe Arg Thr Trp Phe Ile Asp Leu Trp Asn Asn Ser Ile
 420 425 430
 Ile Pro Tyr Leu Gln Glu Gly Ala Lys Asp Gly Ile Lys Val His Gly
 435 440 445
 Gln Lys Ala Ala Trp Glu Asp Pro Val Glu Trp Val Arg Asp Thr Leu
 450 455 460
 Pro Trp Pro Ser Ala Gln Gln Asp Gln Ser Lys Leu Tyr His Leu Pro
 465 470 475 480
 Pro Pro Thr Val Gly Pro His Ser Ile Ala Ser Pro Pro Glu Asp Arg
 485 490 495

Corrected Sequence Listing2.ST25

Thr Val Lys Asp Ser Thr Pro Ser Ser Leu Asp Ser Asp Pro Leu Met
500 505 510

Ala Met Leu Leu Lys Leu Gln Glu Ala Ala Asn Tyr Ile Glu Ser Pro
515 520 525

Asp Arg Glu Thr Ile Leu Asp Pro Asn Leu Gln Ala Thr Leu
530 535 540

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<212> DNA
<213> Mouse

<220>
<221> CDS
<222> (1)..(1695)
<223>

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1 5 10 15
ctc aac tct gcc cac cag ctg gac cag ctt cgg gag acc atg cac aat 96
Leu Asn Ser Ala His Gln Leu Asp Gln Leu Arg Glu Thr Met His Asn
20 25 30
atg cag ttg gag gtg gac ctg ctg aaa gca gag aat gac cgg ctg aag 144
Met Gln Leu Glu Val Asp Leu Leu Lys Ala Glu Asn Asp Arg Leu Lys
35 40 45
gtt gcc ccc ggc ccc tcc tca ggc tgc act cca ggg cag gtc cct ggg 192
Val Ala Pro Gly Pro Ser Ser Gly Cys Thr Pro Gly Gln Val Pro Gly
50 55 60
tca tcg gct ctg tcg tcc cct cga cgt tcc ctg ggc ctt gca ctc agc 240
Ser Ser Ala Leu Ser Ser Pro Arg Arg Ser Leu Gly Leu Ala Leu Ser
65 70 75 80
cat cct ttc agt cct agt ctc aca gac aca gac ctc tca ccc atg gat 288
His Pro Phe Ser Pro Ser Leu Thr Asp Thr Asp Leu Ser Pro Met Asp
85 90 95
ggc atc agc acc tgt ggt tca aag gaa gag gtg acc ctg cgg gtg gtg 336
Gly Ile Ser Thr Cys Gly Ser Lys Glu Glu Val Thr Leu Arg Val Val
100 105 110
gtc cgg atg ccg ccc cag cac atc atc aaa ggg gac tta aag cag cag 384
Val Arg Met Pro Pro Gln His Ile Ile Lys Gly Asp Leu Lys Gln Gln
115 120 125
gag ttc ttc ctg ggt tgc agc aag gtc agt ggc aaa gtt gac tgg aag 432
Glu Phe Phe Leu Gly Cys Ser Lys Val Ser Gly Lys Val Asp Trp Lys
130 135 140
atg ctg gat gaa gcc gtt ttc caa gtg ttc aag gac tac att tct aaa 480
Met Leu Asp Glu Ala Val Phe Gln Val Phe Lys Asp Tyr Ile Ser Lys
145 150 155 160

Corrected Sequence Listing2.ST25

atg gac cca gcc tca acc ctg gga ctg agc act gag tcc ata cat ggc Met Asp Pro Ala Ser Thr Leu Gly Leu Ser Thr Glu Ser Ile His Gly 165 170 175	528
tat agc ctc agc cac gtg aaa cga gtg ctg gat gct gag ccc cca gag Tyr Ser Leu Ser His Val Lys Arg Val Leu Asp Ala Glu Pro Pro Glu 180 185 190	576
atg cct cct tgc cgc cga ggt gtc aat aac ata tca gtc gct ctc aaa Met Pro Pro Cys Arg Arg Gly Val Asn Asn Ile Ser Val Ala Leu Lys 195 200 205	624
ggt ctg aaa gag aag tgt gtc gac agc ctg gtg ttc gag acg ctt atc Gly Leu Lys Glu Lys Cys Val Asp Ser Leu Val Phe Glu Thr Leu Ile 210 215 220	672
ccc aag ccc atg atg cag cac tac atc agc ctc ctg ctc aag cac cgg Pro Lys Pro Met Met Gln His Tyr Ile Ser Leu Leu Lys His Arg 225 230 235 240	720
cgc ctg gtg ctc tcc ggc ccc agt ggc acc ggc aag acc tac ttg acc Arg Leu Val Leu Ser Gly Pro Ser Gly Thr Gly Lys Thr Tyr Leu Thr 245 250 255	768
aat cgg cta gcc gag tac ctg gtg gag cgc tcc ggc cgc gag gtc acg Asn Arg Leu Ala Glu Tyr Leu Val Glu Arg Ser Gly Arg Glu Val Thr 260 265 270	816
gat ggc atc gtc agc act ttc aac atg cac cag cag tct tgc aag gat Asp Gly Ile Val Ser Thr Phe Asn Met His Gln Gln Ser Cys Lys Asp 275 280 285	864
ctg caa ctg tac ctc tcc aac cta gcc aac cag ata gac cgg gaa aca Leu Gln Leu Tyr Leu Ser Asn Leu Ala Asn Gln Ile Asp Arg Glu Thr 290 295 300	912
ggg ata ggg gat gtg ccc ttg gtg atc ctc ctg gat gat ctg agt gaa Gly Ile Gly Asp Val Pro Leu Val Ile Leu Leu Asp Asp Leu Ser Glu 305 310 315 320	960
gca ggc tcc atc agt gag ctg gtc aat ggg gcc ctc acc tgc aag tat Ala Gly Ser Ile Ser Glu Leu Val Asn Gly Ala Leu Thr Cys Lys Tyr 325 330 335	1008
cac aaa tgt ccc tac att ata ggt acc acc aat cag cct gta aaa atg His Lys Cys Pro Tyr Ile Ile Gly Thr Thr Asn Gln Pro Val Lys Met 340 345 350	1056
aca ccc aac cat ggc ttg cac ttg agc ttc agg atg ctg acc ttc tcg Thr Pro Asn His Gly Leu His Leu Ser Phe Arg Met Leu Thr Phe Ser 355 360 365	1104
aac aat gtg gaa cca gcc aat ggc ttt ctg gtc cgt tac ctg cgg agg Asn Asn Val Glu Pro Ala Asn Gly Phe Leu Val Arg Tyr Leu Arg Arg 370 375 380	1152
aag ttg gta gag tca gac agt gac gtc aat gct aac aag gaa gag ctg Lys Leu Val Glu Ser Asp Ser Asp Val Asn Ala Asn Lys Glu Glu Leu 385 390 395 400	1200
ctt cgg gtg ctg gac tgg gtg ccc aag ctg tgg tat cac ctc cac acc Leu Arg Val Leu Asp Trp Val Pro Lys Leu Trp Tyr His Leu His Thr 405 410 415 420	1248

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405	410	415	
ttc ctg gag aag cac agc acc tcg gac ttc ctc att ggc cct tgc ttc Phe Leu Glu Lys His Ser Thr Ser Asp Phe Leu Ile Gly Pro Cys Phe 420 425 430			1296
ttc ctg tcc tgt ccc att ggc atc gag gac ttc cgg acc tgg ttc att Phe Leu Ser Cys Pro Ile Gly Ile Glu Asp Phe Arg Thr Trp Phe Ile 435 440 445			1344
gac ctg tgg aac aat tcc atc atc ccc tat cta cag gaa gga gcc aag Asp Leu Trp Asn Asn Ser Ile Ile Pro Tyr Leu Gln Glu Gly Ala Lys 450 455 460			1392
gat ggg atc aag gtt cat gga cag aaa gct gct tgg gaa gac ccg gtg Asp Gly Ile Lys Val His Gly Gln Lys Ala Ala Trp Glu Asp Pro Val 465 470 475 480			1440
gaa tgg gtc cga gac act ctt ccc tgg ccg tcg gcc caa caa gac caa Glu Trp Val Arg Asp Thr Leu Pro Trp Pro Ser Ala Gln Gln Asp Gln 485 490 495			1488
tca aag ctc tac cac ctg ccc ccg cct tct gtg ggc ccc cac agc act Ser Lys Leu Tyr His Leu Pro Pro Pro Ser Val Gly Pro His Ser Thr 500 505 510			1536
gcc tca ccc ccg gag gac agg aca gtc aaa gac agc act cca aac tcc Ala Ser Pro Pro Glu Asp Arg Thr Val Lys Asp Ser Thr Pro Asn Ser 515 520 525			1584
ctc gac tca gat ccc ctg atg gcc atg cta ctg aaa ctc caa gaa gct Leu Asp Ser Asp Pro Leu Met Ala Met Leu Leu Lys Leu Gln Glu Ala 530 535 540			1632
gcc aac tac att gag tca cca gat cga gag act atc ctg gac ccc aac Ala Asn Tyr Ile Glu Ser Pro Asp Arg Glu Thr Ile Leu Asp Pro Asn 545 550 555 560			1680
ctc cag gcg aca ctc tgagggcccg gcagtcactg tcaccctgga gggcagaagg Leu Gln Ala Thr Leu 565			1735
ctggcttcag catcattagc tctcctctgc cctcttcctt catagctctg gctcaccagc			1795
ctcgccaaga gaacaggagg gaagaagagg gcaggaggag ggatgggttc tcggtgctga			1855
acctttgaga acttcctact aggaattgga gggggtggag tttgagaact ccgtgccctt			1915
taactacatt tgctggcctc ctcttacgac ttaggagaaa agatgattct ggtcttttct			1975
tcaagttttg tttcacctac aaactcttgg gctttctggg gagggattcg gaagatataa			2035
acagacaaac aaaaacaaac aaaccaacta cagcagttcc aagctcgttc tcacaaacac			2095
ctctgagaca gtcacatgtg ggcaaatcta agggaggcag gaagctctac agactttctt			2155
gcaaaccctt cccagttctg tcgacactgc caacaacctc cccgccagag acctggccag			2215
agccaagaaa agagaagcat gtggtttaac agaaaaacaa aacaaaaacaa aacaaaaaat			2275
atatgtgtaa atcaacctgt agaaggtaaa aacggcaatg gaaaagatga agctggaagg			2335
aggggcccag ttgccaagat ggaacgagag ctgccagatc ttgccttctg gatgacaaga			2395

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ggggacattg caagatggct gccagtctaa aacgtcacca gaccacaaga gtaacatcac 2455
agccttcgaa gaaaggccac aagctgtctt tctgccctct aactgaacat gcatgaaaag 2515
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<210> 8
<211> 565
<212> PRT
<213> Mouse

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<400> 8

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Glu Leu Trp Glu Lys Glu Met Lys Leu Thr Asp Ile Arg Leu Glu Ala
1 5 10 15

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Leu Asn Ser Ala His Gln Leu Asp Gln Leu Arg Glu Thr Met His Asn
20 25 30

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Met Gln Leu Glu Val Asp Leu Leu Lys Ala Glu Asn Asp Arg Leu Lys
35 40 45

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Val Ala Pro Gly Pro Ser Ser Gly Cys Thr Pro Gly Gln Val Pro Gly
50 55 60

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Ser Ser Ala Leu Ser Ser Pro Arg Arg Ser Leu Gly Leu Ala Leu Ser
65 70 75 80

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His Pro Phe Ser Pro Ser Leu Thr Asp Thr Asp Leu Ser Pro Met Asp
85 90 95

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Gly Ile Ser Thr Cys Gly Ser Lys Glu Glu Val Thr Leu Arg Val Val
100 105 110

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Val Arg Met Pro Pro Gln His Ile Ile Lys Gly Asp Leu Lys Gln Gln
115 120 125

```

```

Glu Phe Phe Leu Gly Cys Ser Lys Val Ser Gly Lys Val Asp Trp Lys
130 135 140

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```

Met Leu Asp Glu Ala Val Phe Gln Val Phe Lys Asp Tyr Ile Ser Lys
145 150 155 160

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Met Asp Pro Ala Ser Thr Leu Gly Leu Ser Thr Glu Ser Ile His Gly
165 170 175

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Tyr Ser Leu Ser His Val Lys Arg Val Leu Asp Ala Glu Pro Pro Glu
180 185 190

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Corrected Sequence Listing2.ST25

Met Pro Pro Cys Arg Arg Gly Val Asn Asn Ile Ser Val Ala Leu Lys
195 200 205

Gly Leu Lys Glu Lys Cys Val Asp Ser Leu Val Phe Glu Thr Leu Ile
210 215 220

Pro Lys Pro Met Met Gln His Tyr Ile Ser Leu Leu Leu Lys His Arg
225 230 235 240

Arg Leu Val Leu Ser Gly Pro Ser Gly Thr Gly Lys Thr Tyr Leu Thr
245 250 255

Asn Arg Leu Ala Glu Tyr Leu Val Glu Arg Ser Gly Arg Glu Val Thr
260 265 270

Asp Gly Ile Val Ser Thr Phe Asn Met His Gln Gln Ser Cys Lys Asp
275 280 285

Leu Gln Leu Tyr Leu Ser Asn Leu Ala Asn Gln Ile Asp Arg Glu Thr
290 295 300

Gly Ile Gly Asp Val Pro Leu Val Ile Leu Leu Asp Asp Leu Ser Glu
305 310 315 320

Ala Gly Ser Ile Ser Glu Leu Val Asn Gly Ala Leu Thr Cys Lys Tyr
325 330 335

His Lys Cys Pro Tyr Ile Ile Gly Thr Thr Asn Gln Pro Val Lys Met
340 345 350

Thr Pro Asn His Gly Leu His Leu Ser Phe Arg Met Leu Thr Phe Ser
355 360 365

Asn Asn Val Glu Pro Ala Asn Gly Phe Leu Val Arg Tyr Leu Arg Arg
370 375 380

Lys Leu Val Glu Ser Asp Ser Asp Val Asn Ala Asn Lys Glu Glu Leu
385 390 395 400

Leu Arg Val Leu Asp Trp Val Pro Lys Leu Trp Tyr His Leu His Thr
405 410 415

Phe Leu Glu Lys His Ser Thr Ser Asp Phe Leu Ile Gly Pro Cys Phe
420 425 430

Phe Leu Ser Cys Pro Ile Gly Ile Glu Asp Phe Arg Thr Trp Phe Ile
435 440 445

Corrected Sequence Listing2.ST25

Asp Leu Trp Asn Asn Ser Ile Ile Pro Tyr Leu Gln Glu Gly Ala Lys
450 455 460

Asp Gly Ile Lys Val His Gly Gln Lys Ala Ala Trp Glu Asp Pro Val
465 470 475 480

Glu Trp Val Arg Asp Thr Leu Pro Trp Pro Ser Ala Gln Gln Asp Gln
485 490 495

Ser Lys Leu Tyr His Leu Pro Pro Pro Ser Val Gly Pro His Ser Thr
500 505 510

Ala Ser Pro Pro Glu Asp Arg Thr Val Lys Asp Ser Thr Pro Asn Ser
515 520 525

Leu Asp Ser Asp Pro Leu Met Ala Met Leu Leu Lys Leu Gln Glu Ala
530 535 540

Ala Asn Tyr Ile Glu Ser Pro Asp Arg Glu Thr Ile Leu Asp Pro Asn
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Leu Gln Ala Thr Leu
565

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<211> 1025
<212> DNA
<213> Mouse

<220>
<221> CDS
<222> (1)..(129)
<223>

<400> 9
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Pro Ile Glu Leu Arg Ile Lys Arg Gln Asn Ser Ser Asp Ser Ile Ser
1 5 10 15

agc ctc aac agc atc acc agc cat tcc agc atc ggc agc agc aaa gat 96
Ser Leu Asn Ser Ile Thr Ser His Ser Ser Ile Gly Ser Ser Lys Asp
20 25 30

gct gat gcc aag aag aaa aag aag aag agt tgg gtatgtaaag gcttggggat 149
Ala Asp Ala Lys Lys Lys Lys Lys Lys Ser Trp
35 40

cggcctgtgc taggagtcac tcaccctggt gcaggggaact gacccttttc aggatcaaca 209

aagaggggtcc cttctaacag gatgccagtg ttgtgacatc tgctggggac aaaaattcac 269

taagtccca ttctctatc cattgtctat tctccttacc accgccctgc acatataccc 329

cagcccccca ccgtccctgc atcctttata catgtctgct atcctggggc tctacctact 389

Corrected Sequence Listing2.ST25

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gatgagggtca aatgtatttg gccgtagaag gagctgagaa aattattcat ggggtgggaga 449
gtggggcatg tggagagaat ttgtaagcca agcaggggtac tctagacgct cctggggctg 509
ttgcttttagt ttgggtgagg aggctgtgga acgtcccat cgctccaaag cctgcttttg 569
tctgggtccag aggtgggttt gttctgtgtg gtatccccc tgtaactcta aactggcttt 629
gggtgagctt tctacaatct gtacgcaggt gtagggcact gcctgactga ctgaaaggga 689
gagtgacca gagtgagcgt cttgtccctg tccctgctga ggagggctgg ctacagactt 749
tggcctagtg cagacaggag ccagctgtgt ggagaagcag ctgtgtgaaa tgcattgagta 809
gtgtcgtctg tgctgctgct gctgctttct tttcattgtt tttttttttt tttctttcct 869
tttatttcct tcaaatgct gacctcaat ccctattttt tttccagggt tatgaggtaa 929
gaaactcggg tcctctctc gtgctttttc tttccctttg cacaccttcg tgtttccaga 989
gcaagcacct ctcttaaaaa aaaaaaaaaa aaaaaa 1025

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<210> 10
<211> 43
<212> PRT
<213> Mouse

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<400> 10

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Pro Ile Glu Leu Arg Ile Lys Arg Gln Asn Ser Ser Asp Ser Ile Ser
1           5           10          15

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Ser Leu Asn Ser Ile Thr Ser His Ser Ser Ile Gly Ser Ser Lys Asp
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Ala Asp Ala Lys Lys Lys Lys Lys Lys Ser Trp
      35          40

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<210> 11
<211> 8690
<212> DNA
<213> Homo sapiens

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<220>
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<222> (503)..(6187)
<223>

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cgcaaacctg aggatttccg cggcccgccg gcaagacctc ggccagggtt acaggaaatc 180
tgtcattttt tattaataatg gaaaactgtg aagaaagaaa aagatagcag ttgaagtcaa 240
aattctcggg tgactatttt gcttttgagg agtcagcatt taaaaacgat atgctgattt 300

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Corrected Sequence Listing2.ST25

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atcattccctt ggagtcgatg aagttcggaa acggtgtgtg atggggaacg tggcgggcca	420
gtgtgttcct agaaattgca tcttggatta gtttgctgct tttttgaaga gattccattt	480
tgaagggcaa gaacctaatg tg atg gat tta tct tca gaa atg aac aga cat	532
Met Asp Leu Ser Ser Glu Met Asn Arg His	
1 5 10	
ggg aag aat cca gtg agt cac aag cta gaa gat cag aag aag att tac	580
Gly Lys Asn Pro Val Ser His Lys Leu Glu Asp Gln Lys Lys Ile Tyr	
15 20 25	
act gac tgg gcc aac cac tac cta gca aaa tca ggc cac aag cgg ctg	628
Thr Asp Trp Ala Asn His Tyr Leu Ala Lys Ser Gly His Lys Arg Leu	
30 35 40	
atc aag gac ttg caa caa gac att gca gat gga gta ctc cta gca gaa	676
Ile Lys Asp Leu Gln Gln Asp Ile Ala Asp Gly Val Leu Leu Ala Glu	
45 50 55	
atc atc cag att att gca aat gaa aaa gtt gaa gat atc aat gga tgt	724
Ile Ile Gln Ile Ile Ala Asn Glu Lys Val Glu Asp Ile Asn Gly Cys	
60 65 70	
cct aga agt cag tct cag atg att gaa aat gtt gat gtc tgc ctt agt	772
Pro Arg Ser Gln Ser Gln Met Ile Glu Asn Val Asp Val Cys Leu Ser	
75 80 85 90	
ttt cta gca gcc aga ggg gta aat gtt caa ggt cta tct gct gaa gaa	820
Phe Leu Ala Ala Arg Gly Val Asn Val Gln Gly Leu Ser Ala Glu Glu	
95 100 105	
ata aga aat gga aac tta aaa gcc att cta ggg ctg ttt ttc agt tta	868
Ile Arg Asn Gly Asn Leu Lys Ala Ile Leu Gly Leu Phe Phe Ser Leu	
110 115 120	
tct cgc tac aag cag caa caa cac cat caa caa cag tac tat cag tcc	916
Ser Arg Tyr Lys Gln Gln Gln His His Gln Gln Gln Tyr Tyr Gln Ser	
125 130 135	
ttg gtg gaa ctt cag cag cga gtt act cac gct tcc cct cca tcg gaa	964
Leu Val Glu Leu Gln Gln Arg Val Thr His Ala Ser Pro Pro Ser Glu	
140 145 150	
gcc agc cag gcc aaa acc cag caa gat atg cag tcc agg ctt cca ggg	1012
Ala Ser Gln Ala Lys Thr Gln Gln Asp Met Gln Ser Arg Leu Pro Gly	
155 160 165 170	
ccc tct agg gtg cct gct gca gga agc agc agc aag gtc cag gga gcc	1060
Pro Ser Arg Val Pro Ala Ala Gly Ser Ser Ser Lys Val Gln Gly Ala	
175 180 185	
tct aat tta aat agg aga agt cag agc ttt aac agc att gac aaa aac	1108
Ser Asn Leu Asn Arg Arg Ser Gln Ser Phe Asn Ser Ile Asp Lys Asn	
190 195 200	
aag cct cca aat tat gca aat gga aac gaa aaa ggt gaa gac cct gaa	1156
Lys Pro Pro Asn Tyr Ala Asn Gly Asn Glu Lys Gly Glu Asp Pro Glu	
205 210 215	

Corrected Sequence Listing2.ST25

aca Thr	aga Arg	aga Arg	atg Met	aga Arg	aca Thr	ggt Val	aaa Lys	aac Asn	ata Ile	gca Ala	gac Asp	ttg Leu	agg Arg	cag Gln	aat Asn	1204
220						225					230					
tta Leu	gaa Glu	gag Glu	act Thr	atg Met	tcc Ser	agt Ser	ctt Leu	cgt Arg	ggg Gly	act Thr	cag Gln	ata Ile	agc Ser	cac His	agc Ser	1252
235					240					245					250	
acc Thr	ctg Leu	gag Glu	aca Thr	aca Thr	ttt Phe	gac Asp	agc Ser	act Thr	gtg Val	aca Thr	aca Thr	gaa Glu	gtt Val	aat Asn	gga Gly	1300
				255					260					265		
agg Arg	acc Thr	ata Ile	ccc Pro	aac Asn	ttg Leu	aca Thr	agt Ser	cga Arg	ccc Pro	acc Thr	ccc Pro	atg Met	acc Thr	tgg Trp	agg Arg	1348
			270					275				280				
ttg Leu	ggc Gly	cag Gln	gca Ala	tgt Cys	ccg Pro	cga Arg	ctt Leu	cag Gln	gcg Ala	gga Gly	gat Asp	gct Ala	ccc Pro	tcc Ser	ctg Leu	1396
		285					290					295				
ggt Gly	gct Ala	ggc Gly	tat Tyr	cct Pro	cgc Arg	agt Ser	ggt Gly	acc Thr	agt Ser	cga Arg	ttc Phe	atc Ile	cac His	aca Thr	gac Asp	1444
	300					305					310					
ccc Pro	tcg Ser	agg Arg	ttc Phe	atg Met	tat Tyr	acc Thr	acg Thr	cct Pro	ctc Leu	cgt Arg	cga Arg	gct Ala	gct Ala	gtc Val	tct Ser	1492
315					320					325					330	
agg Arg	ctg Leu	gga Gly	aac Asn	atg Met	tca Ser	cag Gln	att Ile	gac Asp	atg Met	agt Ser	gag Glu	aaa Lys	gca Ala	agc Ser	agt Ser	1540
				335					340					345		
gac Asp	ctg Leu	gac Asp	atg Met	tct Ser	tct Ser	gag Glu	gtc Val	gat Asp	gtg Val	ggt Gly	gga Gly	tat Tyr	atg Met	agt Ser	gat Asp	1588
			350					355					360			
ggt Gly	gat Asp	atc Ile	ctt Leu	ggg Gly	aaa Lys	agt Ser	ctc Leu	agg Arg	act Thr	gat Asp	gac Asp	atc Ile	aac Asn	agt Ser	ggg Gly	1636
		365					370					375				
tac Tyr	atg Met	aca Thr	gat Asp	gga Gly	gga Gly	ctt Leu	aac Asn	cta Leu	tat Tyr	act Thr	aga Arg	agt Ser	ctg Leu	aac Asn	cga Arg	1684
	380					385					390					
ata Ile	cca Pro	gac Asp	aca Thr	gca Ala	act Thr	tcc Ser	cgg Arg	gac Asp	atc Ile	atc Ile	cag Gln	aga Arg	ggg Gly	gtt Val	cac His	1732
395					400					405					410	
gat Asp	gtg Val	aca Thr	gtg Val	gat Asp	gca Ala	gac Asp	agc Ser	tgg Trp	gat Asp	gac Asp	agc Ser	agt Ser	tca Ser	gtg Val	agc Ser	1780
				415					420					425		
agt Ser	ggt Gly	ctc Leu	agt Ser	gac Asp	acc Thr	ctt Leu	gat Asp	aac Asn	atc Ile	agc Ser	act Thr	gat Asp	gac Asp	ctg Leu	aac Asn	1828
				430				435					440			
acc Thr	aca Thr	tcc Ser	tct Ser	gtc Val	agc Ser	tct Ser	tac Tyr	tcc Ser	aac Asn	atc Ile	acc Thr	gtc Val	ccc Pro	tct Ser	agg Arg	1876
		445					450					455				
aag Lys	aat Asn	act Thr	cag Gln	ctg Leu	agg Arg	aca Thr	gat Asp	tca Ser	gag Glu	aaa Lys	cgc Arg	tcc Ser	acc Thr	aca Thr	gac Asp	1924
	460					465					470					

Corrected Sequence Listing2.ST25

gag Glu 475	acc Thr	tgg Trp	gat Asp	agt Ser	cct Pro 480	gag Glu	gaa Glu	ctg Leu	aaa Lys	aaa Lys 485	cca Pro	gaa Glu	gaa Glu	gat Asp	ttt Phe 490	1972
gac Asp	agc Ser	cat His	ggg Gly 495	gat Asp	gct Ala	ggt Gly	ggc Gly	aag Lys	tgg Trp 500	aag Lys	act Thr	gtg Val	tcc Ser	tct Ser 505	gga Gly	2020
ctt Leu	cct Pro	gaa Glu	gac Asp 510	ccc Pro	gag Glu	aag Lys	gca Ala	ggg Gly 515	cag Gln	aaa Lys	gct Ala	tcc Ser	ctg Leu 520	tct Ser	gtt Val	2068
tca Ser	cag Gln 525	aca Thr	ggt Gly	tcc Ser	tgg Trp	aga Arg	aga Arg 530	ggc Gly	atg Met	tct Ser	gcc Ala	caa Gln 535	gga Gly	ggg Gly	gcg Ala	2116
cca Pro 540	tct Ser	agg Arg	cag Gln	aaa Lys	gct Ala	gga Gly 545	aca Thr	agt Ser	gca Ala	ctc Leu 550	aaa Lys	aca Thr	ccc Pro	ggg Gly	aaa Lys	2164
acc Thr 555	gat Asp	gat Asp	gcc Ala	aaa Lys	gct Ala 560	tct Ser	gag Glu	aaa Lys	gga Gly 565	aaa Lys	gct Ala	ccc Pro	cta Leu	aaa Lys	gga Gly 570	2212
tca Ser	tct Ser	cta Leu	caa Gln 575	aga Arg	tct Ser	cct Pro	tca Ser	gat Asp	gca Ala 580	gga Gly	aaa Lys	agc Ser	agt Ser	gga Gly 585	gat Asp	2260
gaa Glu	ggg Gly	aaa Lys 590	aag Lys	ccc Pro	ccc Pro	tca Ser	ggc Gly	att Ile 595	gga Gly	aga Arg	tcg Ser	act Thr	gcc Ala 600	acc Thr	agc Ser	2308
tcc Ser	ttt Phe 605	ggc Gly	ttt Phe	aag Lys	aaa Lys	cca Pro	agt Ser 610	gga Gly	gta Val	ggg Gly	tca Ser	tct Ser 615	gcc Ala	atg Met	atc Ile	2356
acc Thr 620	agc Ser	agt Ser	gga Gly	gca Ala	acc Thr	ata Ile 625	aca Thr	agt Ser	ggc Gly	tct Ser	gca Ala 630	aca Thr	ctg Leu	ggt Gly	aaa Lys	2404
att Ile 635	cca Pro	aaa Lys	tct Ser	gct Ala	gcc Ala 640	att Ile	ggc Gly	ggg Gly	aag Lys	tca Ser 645	aat Asn	gca Ala	ggg Gly	aga Arg	aaa Lys 650	2452
acc Thr	agt Ser	ttg Leu	gac Asp 655	ggt Gly	tca Ser	cag Gln	aat Asn	cag Gln	gat Asp 660	gat Asp	gtt Val	gtg Val	ctg Leu	cat His 665	gtt Val	2500
agc Ser	tca Ser	aag Lys	act Thr 670	acc Thr	cta Leu	caa Gln	tat Tyr	cgc Arg 675	agc Ser	ttg Leu	ccc Pro	cgc Arg	cct Pro 680	tca Ser	aaa Lys	2548
tcc Ser	agc Ser	acc Thr 685	agt Ser	ggc Gly	att Ile	cct Pro	ggc Gly 690	cga Arg	gga Gly	ggc Gly	cac His	aga Arg 695	tcc Ser	agt Ser	acc Thr	2596
agc Ser 700	agt Ser	att Ile	gat Asp	tcc Ser	aac Asn	gtc Val 705	agc Ser	agc Ser	aag Lys	tct Ser	gct Ala 710	ggg Gly	gcc Ala	acc Thr	acc Thr	2644
tcg Ser	aaa Lys	ctg Leu	aga Arg	gaa Glu	cca Pro	act Thr	aaa Lys	att Ile	ggg Gly	tca Ser	ggg Gly	cgc Arg	tcg Ser	agt Ser	cct Pro	2692

Corrected Sequence Listing2.ST25

715		720		725		730										
gtc Val	acc Thr	gtc Val	aac Asn	caa Gln 735	aca Thr	gac Asp	aag Lys	gaa Glu	aag Lys 740	gaa Glu	aaa Lys	gta Val	gca Ala	gtc Val 745	tca Ser	2740
gat Asp	tca Ser	gaa Glu	agt Ser 750	ggt Val	tct Ser	ttg Leu	tca Ser	ggt Gly 755	tcc Ser	ccc Pro	aaa Lys	tcc Ser	agc Ser 760	ccc Pro	acc Thr	2788
tct Ser	gcc Ala	agc Ser 765	gcc Ala	tgt Cys	ggt Gly	gca Ala	caa Gln 770	ggt Gly	ctc Leu	agg Arg	cag Gln	cca Pro 775	gga Gly	tcc Ser	aag Lys	2836
tat Tyr	cca Pro 780	gat Asp	att Ile	gcc Ala	tca Ser	ccc Pro 785	aca Thr	ttt Phe	cga Arg	agg Arg	ttg Leu 790	ttt Phe	ggt Gly	gcc Ala	aag Lys	2884
gca Ala 795	ggt Gly	ggc Gly	aaa Lys	tct Ser	gcc Ala 800	tct Ser	gca Ala	cct Pro	aat Asn	act Thr 805	gag Glu	ggt Gly	gtg Val	aaa Lys	tct Ser 810	2932
tcc Ser	tca Ser	gta Val	atg Met	ccc Pro 815	agc Ser	cct Pro	agt Ser	acc Thr	aca Thr 820	tta Leu	gcg Ala	cgg Arg	caa Gln	ggc Gly 825	agt Ser	2980
ctg Leu	gag Glu	tca Ser	ccg Pro 830	tcg Ser	tcc Ser	ggt Gly	acg Thr	ggc Gly 835	agc Ser	atg Met	ggc Gly	agt Ser	gct Ala 840	ggt Gly	ggg Gly	3028
cta Leu	agc Ser	ggc Gly 845	agc Ser	agc Ser	agc Ser	cct Pro	ctc Leu 850	ttc Phe	aat Asn	aaa Lys	ccc Pro	tca Ser 855	gac Asp	tta Leu	act Thr	3076
aca Thr	gat Asp 860	gtt Val	ata Ile	agc Ser	tta Leu	agt Ser 865	cac His	tcg Ser	ttg Leu	gcc Ala	tcc Ser 870	agc Ser	cca Pro	gca Ala	tcg Ser	3124
gtt Val 875	cac His	tct Ser	ttc Phe	aca Thr	tca Ser 880	ggt Gly	ggt Gly	ctc Leu	gtg Val	tgg Trp 885	gct Ala	gcc Ala	aat Asn	atg Met	agc Ser 890	3172
agt Ser	tcc Ser	tct Ser	gca Ala	ggc Gly 895	agc Ser	aag Lys	gat Asp	act Thr	ccg Pro 900	agc Ser	tac Tyr	cag Gln	tcc Ser	atg Met 905	act Thr	3220
agc Ser	ctc Leu	cac His	acg Thr 910	agc Ser	tct Ser	gag Glu	tcc Ser	att Ile 915	gac Asp	ctc Leu	ccc Pro	ctc Leu	agc Ser 920	cat His	cat His	3268
ggc Gly	tcc Ser	ttg Leu 925	tct Ser	gga Gly	ctg Leu	acc Thr	aca Thr 930	ggc Gly	act Thr	cac His	gag Glu	gtc Val 935	cag Gln	agc Ser	ctg Leu	3316
ctc Leu	atg Met 940	aga Arg	acg Thr	ggt Gly	agt Ser	gtg Val 945	aga Arg	tct Ser	act Thr	ctc Leu	tca Ser 950	gaa Glu	agc Ser	atg Met	cag Gln	3364
ctt Leu 955	gac Asp	aga Arg	aat Asn	aca Thr	cta Leu 960	ccc Pro	aaa Lys	aag Lys	gga Gly	cta Leu 965	aga Arg	tat Tyr	acc Thr	cca Pro	tca Ser 970	3412
tct	cgg	cag	gcc	aac	caa	gaa	gag	ggc	aaa	gag	tgg	ttg	cgt	tct	cat	3460

Corrected Sequence Listing2.ST25

ser	arg	gln	ala	asn	gln	glu	glu	gly	lys	glu	trp	leu	arg	ser	his		
				975					980					985			
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ser	thr	gly	gly	leu	gln	asp	thr	gly	asn	gln	ser	pro	leu	val	ser		
			990					995					1000				
cct	tct	gcc	atg	tca	tct	tct	gca	gct	gga	aaa	tac	cac	ttt	tct		3553	
pro	ser	ala	met	ser	ser	ser	ala	ala	gly	lys	tyr	his	phe	ser			
		1005					1010					1015					
aac	ttg	gtg	agc	cca	aca	aat	ttg	tct	caa	ttt	aac	ctt	ccc	ggg		3598	
asn	leu	val	ser	pro	thr	asn	leu	ser	gln	phe	asn	leu	pro	gly			
		1020					1025					1030					
ccc	agc	atg	atg	cgc	tca	aac	agc	atc	cca	gcc	caa	gac	tct	tcc		3643	
pro	ser	met	met	arg	ser	asn	ser	ile	pro	ala	gln	asp	ser	ser			
		1035					1040					1045					
ttc	gat	ctc	tat	gat	gac	tcc	cag	ctt	tgt	ggg	agt	gcc	act	tct		3688	
phe	asp	leu	tyr	asp	asp	ser	gln	leu	cys	gly	ser	ala	thr	ser			
		1050					1055					1060					
ctg	gag	gaa	aga	cct	cgt	gcc	atc	agt	cat	tcg	ggc	tca	ttc	aga		3733	
leu	glu	glu	arg	pro	arg	ala	ile	ser	his	ser	gly	ser	phe	arg			
		1065					1070					1075					
gac	agc	atg	gaa	gaa	gtt	cat	ggc	tct	tca	tta	tca	ctg	gtg	tcc		3778	
asp	ser	met	glu	glu	val	his	gly	ser	ser	leu	ser	leu	val	ser			
		1080					1085					1090					
agc	act	tct	tct	ctt	tac	tct	aca	gct	gaa	gaa	aag	gct	cat	tca		3823	
ser	thr	ser	ser	leu	tyr	ser	thr	ala	glu	glu	lys	ala	his	ser			
		1095					1100					1105					
gag	caa	atc	cat	aaa	ctg	cgg	aga	gag	ctg	gtt	gca	tca	caa	gaa		3868	
glu	gln	ile	his	lys	leu	arg	arg	glu	leu	val	ala	ser	gln	glu			
		1110					1115					1120					
aaa	gtt	gct	acc	ctc	aca	tct	cag	ctt	tca	gca	aat	gct	cac	ctt		3913	
lys	val	ala	thr	leu	thr	ser	gln	leu	ser	ala	asn	ala	his	leu			
		1125					1130					1135					
gta	gca	gct	ttt	gaa	aag	agc	tta	ggg	aat	atg	act	ggc	cga	ttg		3958	
val	ala	ala	phe	glu	lys	ser	leu	gly	asn	met	thr	gly	arg	leu			
		1140					1145					1150					
caa	agt	cta	act	atg	aca	gcg	gaa	caa	aag	gaa	tct	gaa	ctt	ata		4003	
gln	ser	leu	thr	met	thr	ala	glu	gln	lys	glu	ser	glu	leu	ile			
		1155					1160					1165					
gaa	cta	aga	gaa	acc	att	gaa	atg	ctg	aag	gct	cag	aat	tct	gct		4048	
glu	leu	arg	glu	thr	ile	glu	met	leu	lys	ala	gln	asn	ser	ala			
		1170					1175					1180					
gcc	cag	gcg	gct	att	cag	gga	gca	ctg	aat	ggt	cca	gac	cat	cct		4093	
ala	gln	ala	ala	ile	gln	gly	ala	leu	asn	gly	pro	asp	his	pro			
		1185					1190					1195					
ccc	aaa	gat	ctt	cgc	atc	aga	aga	cag	cat	tcc	tct	gaa	agt	gtt		4138	
pro	lys	asp	leu	arg	ile	arg	arg	gln	his	ser	ser	glu	ser	val			
		1200					1205					1210					

Corrected Sequence Listing2.ST25															
tct	agt	atc	aac	agt	gcc	aca	agc	cat	tcc	agt	att	ggc	agt	ggc	4183
Ser	Ser	Ile	Asn	Ser	Ala	Thr	Ser	His	Ser	Ser	Ile	Gly	Ser	Gly	
		1215					1220					1225			
aat	gat	gcc	gac	tcc	aag	aag	aag	aaa	aag	aaa	aac	tgg	ctg	aga	4228
Asn	Asp	Ala	Asp	Ser	Lys	Lys	Lys	Lys	Lys	Lys	Asn	Trp	Leu	Arg	
		1230					1235					1240			
agt	tct	ttc	aaa	caa	gcc	ttt	ggg	aag	aaa	aag	tcc	acc	aag	cct	4273
Ser	Ser	Phe	Lys	Gln	Ala	Phe	Gly	Lys	Lys	Lys	Ser	Thr	Lys	Pro	
		1245					1250					1255			
cct	tca	tca	cat	tct	gac	att	gaa	gag	ctt	act	gat	tca	tcc	ctt	4318
Pro	Ser	Ser	His	Ser	Asp	Ile	Glu	Glu	Leu	Thr	Asp	Ser	Ser	Leu	
		1260					1265					1270			
ccg	gca	tcc	ccc	aag	tta	ccc	cat	aat	gct	ggc	gac	tgt	ggc	tca	4363
Pro	Ala	Ser	Pro	Lys	Leu	Pro	His	Asn	Ala	Gly	Asp	Cys	Gly	Ser	
		1275					1280					1285			
gca	tcc	atg	aag	ccc	tca	caa	tct	gct	tca	gcg	atc	tgt	gaa	tgc	4408
Ala	Ser	Met	Lys	Pro	Ser	Gln	Ser	Ala	Ser	Ala	Ile	Cys	Glu	Cys	
		1290					1295					1300			
aca	gaa	gct	gag	gca	gag	ata	att	ctg	cag	ctg	aag	agc	gag	ctc	4453
Thr	Glu	Ala	Glu	Ala	Glu	Ile	Ile	Leu	Gln	Leu	Lys	Ser	Glu	Leu	
		1305					1310					1315			
aga	gaa	aag	gaa	tta	aaa	tta	acg	gat	att	cgg	ctg	gag	gcc	ctc	4498
Arg	Glu	Lys	Glu	Leu	Lys	Leu	Thr	Asp	Ile	Arg	Leu	Glu	Ala	Leu	
		1320					1325					1330			
agc	tct	gct	cat	cat	ctt	gat	cag	atc	cgg	gaa	gcc	atg	aac	cgg	4543
Ser	Ser	Ala	His	His	Leu	Asp	Gln	Ile	Arg	Glu	Ala	Met	Asn	Arg	
		1335					1340					1345			
atg	cag	aat	gaa	att	gaa	ata	ctg	aaa	gct	gaa	aat	gac	cgg	ttg	4588
Met	Gln	Asn	Glu	Ile	Glu	Ile	Leu	Lys	Ala	Glu	Asn	Asp	Arg	Leu	
		1350					1355					1360			
aag	gca	gaa	act	ggt	aac	aca	gct	aag	cct	act	cgg	cca	ccg	tca	4633
Lys	Ala	Glu	Thr	Gly	Asn	Thr	Ala	Lys	Pro	Thr	Arg	Pro	Pro	Ser	
		1365					1370					1375			
gaa	tcc	tca	agc	agc	acc	tcc	tct	tca	tct	tcc	agg	cag	tca	tta	4678
Glu	Ser	Ser	Ser	Ser	Thr	Ser	Ser	Ser	Ser	Ser	Arg	Gln	Ser	Leu	
		1380					1385					1390			
gga	ctt	tct	cta	aac	aat	ttg	aac	atc	aca	gag	gct	gtt	agc	tca	4723
Gly	Leu	Ser	Leu	Asn	Asn	Leu	Asn	Ile	Thr	Glu	Ala	Val	Ser	Ser	
		1395					1400					1405			
gat	att	ttg	cta	gat	gat	gct	ggt	gat	gca	act	gga	cat	aaa	gat	4768
Asp	Ile	Leu	Leu	Asp	Asp	Ala	Gly	Asp	Ala	Thr	Gly	His	Lys	Asp	
		1410					1415					1420			
ggc	cgc	agt	gtg	aaa	att	ata	gtc	tcc	ata	agc	aag	ggc	tat	ggc	4813
Gly	Arg	Ser	Val	Lys	Ile	Ile	Val	Ser	Ile	Ser	Lys	Gly	Tyr	Gly	
		1425					1430					1435			
cga	gca	aag	gac	caa	aaa	tct	cag	gca	tat	ttg	ata	gga	tcc	att	4858
Arg	Ala	Lys	Asp	Gln	Lys	Ser	Gln	Ala	Tyr	Leu	Ile	Gly	Ser	Ile	
		1440					1445					1450			

Corrected Sequence Listing2.ST25

ggt gtt agt gga aaa acc aag tgg gat gtc tta gat ggt gta ata	4903
Gly Val Ser 1455 Gly Lys Thr Lys Trp 1460 Asp Val Leu Asp Gly 1465 Val Ile	
aga cgt ctc ttt aag gaa tat gta ttc cga att gat aca tcc act	4948
Arg Arg Leu 1470 Phe Lys Glu Tyr Val 1475 Phe Arg Ile Asp Thr 1480 Ser Thr	
agc ctt ggt ctg agc tct gac tgc att gct agc tac tgt ata gga	4993
Ser Leu Gly 1485 Leu Ser Ser Asp Cys 1490 Ile Ala Ser Tyr Cys 1495 Ile Gly	
gac tta att aga tcc cat aac cta gaa gtg cct gaa ttg ctg cct	5038
Asp Leu Ile 1500 Arg Ser His Asn Leu 1505 Glu Val Pro Glu Leu 1510 Leu Pro	
tgt gga tac ctt gtt gga gat aat aac atc atc act gtg aac ctc	5083
Cys Gly Tyr 1515 Leu Val Gly Asp Asn 1520 Asn Ile Ile Thr Val 1525 Asn Leu	
aaa ggg gta gaa gaa aat agt ttg gac agt ttt gtt ttt gat acg	5128
Lys Gly Val 1530 Glu Glu Asn Ser Leu 1535 Asp Ser Phe Val Phe 1540 Asp Thr	
ctg att cct aaa cca att acc caa agg tac ttt aac ttg ttg atg	5173
Leu Ile Pro 1545 Lys Pro Ile Thr Gln 1550 Arg Tyr Phe Asn Leu 1555 Leu Met	
gag cat cac aga att ata ctc tca gga ccg agt ggt act gga aag	5218
Glu His His 1560 Arg Ile Ile Leu Ser 1565 Gly Pro Ser Gly Thr 1570 Gly Lys	
acc tat ttg gca aac aaa ctt gct gaa tat gta ata acc aaa tct	5263
Thr Tyr Leu 1575 Ala Asn Lys Leu Ala 1580 Glu Tyr Val Ile Thr 1585 Lys Ser	
gga agg aaa aaa aca gag gat gca att gcc act ttt aat gtg gac	5308
Gly Arg Lys 1590 Lys Thr Glu Asp Ala 1595 Ile Ala Thr Phe Asn 1600 Val Asp	
cac aag tca agt aag gaa ttg caa caa tat cta gct aac ctg gct	5353
His Lys Ser 1605 Ser Lys Glu Leu Gln 1610 Gln Tyr Leu Ala Asn 1615 Leu Ala	
gaa cag tgc agt gct gat aat aat gga gtg gag ctc cca gtt gta	5398
Glu Gln Cys 1620 Ser Ala Asp Asn Asn 1625 Gly Val Glu Leu Pro 1630 Val Val	
ata att ctt gat aat ctt cat cat gtg ggc tct ctg agt gat atc	5443
Ile Ile Leu 1635 Asp Asn Leu His His 1640 Val Gly Ser Leu Ser 1645 Asp Ile	
ttc aat ggt ttt ctc aat tgt aaa tac aac aaa tgt cca tat att	5488
Phe Asn Gly 1650 Phe Leu Asn Cys Lys 1655 Tyr Asn Lys Cys Pro 1660 Tyr Ile	
att gga aca atg aat cag gga gtt tct tca tca cca aat cta gag	5533
Ile Gly Thr 1665 Met Asn Gln Gly Val 1670 Ser Ser Ser Pro Asn 1675 Leu Glu	
ctg cat cac aat ttc agg tgg gta tta tgt gca aat cat aca gaa	5578
Leu His His Asn Phe Arg Trp Val Leu Cys Ala Asn His Thr Glu	

Corrected Sequence Listing2.ST25

1680	1685	1690	
cca gtg aaa ggc ttt tta ggc aga tat ctt cga aga aaa ctc ata Pro Val Lys Gly Phe Leu Gly Arg Tyr Leu Arg Arg Lys Leu Ile 1695 1700 1705			5623
gag ata gaa att gaa agg aac att cgc aat aat gac cta gtc aaa Glu Ile Glu Ile Glu Arg Asn Ile Arg Asn Asn Asp Leu Val Lys 1710 1715 1720			5668
att ata gat tgg att ccg aag acg tgg cat cat ctc aac agt ttt Ile Ile Asp Trp Ile Pro Lys Thr Trp His His Leu Asn Ser Phe 1725 1730 1735			5713
ttg gaa aca cac agt tct tct gac gtt acc att ggt ccc cga cta Leu Glu Thr His Ser Ser Ser Asp Val Thr Ile Gly Pro Arg Leu 1740 1745 1750			5758
ttc ctt cct tgc ccc atg gat gta gaa ggt tct aga gta tgg ttc Phe Leu Pro Cys Pro Met Asp Val Glu Gly Ser Arg Val Trp Phe 1755 1760 1765			5803
atg gat ctc tgg aac tat tct tta gta cct tat att ctg gag gca Met Asp Leu Trp Asn Tyr Ser Leu Val Pro Tyr Ile Leu Glu Ala 1770 1775 1780			5848
gtg aga gag ggt ctt cag atg tat ggg aaa cgc aca cca tgg gaa Val Arg Glu Gly Leu Gln Met Tyr Gly Lys Arg Thr Pro Trp Glu 1785 1790 1795			5893
gat cct tca aag tgg gtg ctt gac aca tat cca tgg agc tca gca Asp Pro Ser Lys Trp Val Leu Asp Thr Tyr Pro Trp Ser Ser Ala 1800 1805 1810			5938
act ctg cct cag gag agc cca gcc tta ctt cag ctg cga cca gaa Thr Leu Pro Gln Glu Ser Pro Ala Leu Leu Gln Leu Arg Pro Glu 1815 1820 1825			5983
gat gtt ggg tat gaa agc tgc aca tcc act aag gaa gcc aca acc Asp Val Gly Tyr Glu Ser Cys Thr Ser Thr Lys Glu Ala Thr Thr 1830 1835 1840			6028
tca aag cac att cca caa act gac aca gaa gga gat ccc ctg atg Ser Lys His Ile Pro Gln Thr Asp Thr Glu Gly Asp Pro Leu Met 1845 1850 1855			6073
aat atg cta atg aaa ctc caa gaa gca gcc aat tac tcg agc aca Asn Met Leu Met Lys Leu Gln Glu Ala Ala Asn Tyr Ser Ser Thr 1860 1865 1870			6118
caa agc tgc gac agc gaa agc acc agt cac cat gaa gac att ttg Gln Ser Cys Asp Ser Glu Ser Thr Ser His His Glu Asp Ile Leu 1875 1880 1885			6163
gat tca tct ctt gaa tct acc ctc tagagggtga aaaaagttaa Asp Ser Ser Leu Glu Ser Thr Leu 1890 1895			6207
gggaaaagac ttgtctttta aaaaaatgtt tcaaaagaaa ggtatttttca ctaaaccact			6267
gccagtataa aagcaccctg tcaagggcc tgacccagag ttgtgggtctc caaggaggca			6327
gcagaactaa gtctgaaccg ccaagatgct aaattgcaat ggaagcttaa ctttagttta			6387

Corrected Sequence Listing2.ST25

tttctaaaca	ttttttatat	ctgtggagta	atagaaagct	ccattactca	actggaaagg	6447
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taaaacttgc	acaaatcaaa	acaaacacaa	acaaaattgt	attttatcct	gttggtgtta	7647
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taggacgtgt	atgtggtgct	actctctgtg	accaccaatg	ggtcagttgc	tatagaacaa	8067
caacaccacg	aaacatctgt	gcagttttca	gagtgtcaca	aagtcaatag	gtccttacac	8127
ggtgctattg	ccctaagggg	aatccgaact	gaatttatgc	acatagaatt	gtcacctga	8187
ctttgaagcc	tcaaacatgg	atcaaactctg	ttgtgaaaca	tcaatatatg	tagctggatg	8247

Corrected Sequence Listing2.ST25

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agtgactagt ttcccttgta taatatgtga tctaagaaaa ttgctaattct ttccctgcca 8307
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aattatttat tgacaaaaaa aaa 8690

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 <211> 1895
 <212> PRT
 <213> Homo sapiens

<400> 12

Met Asp Leu Ser Ser Glu Met Asn Arg His Gly Lys Asn Pro Val Ser
 1 5 10 15

His Lys Leu Glu Asp Gln Lys Lys Ile Tyr Thr Asp Trp Ala Asn His
 20 25 30

Tyr Leu Ala Lys Ser Gly His Lys Arg Leu Ile Lys Asp Leu Gln Gln
 35 40 45

Asp Ile Ala Asp Gly Val Leu Leu Ala Glu Ile Ile Gln Ile Ile Ala
 50 55 60

Asn Glu Lys Val Glu Asp Ile Asn Gly Cys Pro Arg Ser Gln Ser Gln
 65 70 75 80

Met Ile Glu Asn Val Asp Val Cys Leu Ser Phe Leu Ala Ala Arg Gly
 85 90 95

Val Asn Val Gln Gly Leu Ser Ala Glu Glu Ile Arg Asn Gly Asn Leu
 100 105 110

Lys Ala Ile Leu Gly Leu Phe Phe Ser Leu Ser Arg Tyr Lys Gln Gln
 115 120 125

Gln His His Gln Gln Gln Tyr Tyr Gln Ser Leu Val Glu Leu Gln Gln
 130 135 140

Arg Val Thr His Ala Ser Pro Pro Ser Glu Ala Ser Gln Ala Lys Thr
 145 150 155 160

Corrected Sequence Listing2.ST25

Gln Gln Asp Met Gln Ser Arg Leu Pro Gly Pro Ser Arg Val Pro Ala
165 170 175

Ala Gly Ser Ser Ser Lys Val Gln Gly Ala Ser Asn Leu Asn Arg Arg
180 185 190

Ser Gln Ser Phe Asn Ser Ile Asp Lys Asn Lys Pro Pro Asn Tyr Ala
195 200 205

Asn Gly Asn Glu Lys Gly Glu Asp Pro Glu Thr Arg Arg Met Arg Thr
210 215 220

Val Lys Asn Ile Ala Asp Leu Arg Gln Asn Leu Glu Glu Thr Met Ser
225 230 235 240

Ser Leu Arg Gly Thr Gln Ile Ser His Ser Thr Leu Glu Thr Thr Phe
245 250 255

Asp Ser Thr Val Thr Thr Glu Val Asn Gly Arg Thr Ile Pro Asn Leu
260 265 270

Thr Ser Arg Pro Thr Pro Met Thr Trp Arg Leu Gly Gln Ala Cys Pro
275 280 285

Arg Leu Gln Ala Gly Asp Ala Pro Ser Leu Gly Ala Gly Tyr Pro Arg
290 295 300

Ser Gly Thr Ser Arg Phe Ile His Thr Asp Pro Ser Arg Phe Met Tyr
305 310 315 320

Thr Thr Pro Leu Arg Arg Ala Ala Val Ser Arg Leu Gly Asn Met Ser
325 330 335

Gln Ile Asp Met Ser Glu Lys Ala Ser Ser Asp Leu Asp Met Ser Ser
340 345 350

Glu Val Asp Val Gly Gly Tyr Met Ser Asp Gly Asp Ile Leu Gly Lys
355 360 365

Ser Leu Arg Thr Asp Asp Ile Asn Ser Gly Tyr Met Thr Asp Gly Gly
370 375 380

Leu Asn Leu Tyr Thr Arg Ser Leu Asn Arg Ile Pro Asp Thr Ala Thr
385 390 395 400

Ser Arg Asp Ile Ile Gln Arg Gly Val His Asp Val Thr Val Asp Ala
405 410 415

Corrected Sequence Listing2.ST25

Asp Ser Trp Asp 420 Asp Ser Ser Ser Val 425 Ser Ser Gly Leu Ser 430 Asp Thr
 Leu Asp Asn 435 Ile Ser Thr Asp Asp 440 Leu Asn Thr Thr Ser 445 Ser Val Ser
 Ser Tyr 450 Ser Asn Ile Thr Val 455 Pro Ser Arg Lys Asn 460 Thr Gln Leu Arg
 Thr 465 Asp Ser Glu Lys Arg 470 Ser Thr Thr Asp Glu 475 Thr Trp Asp Ser Pro 480
 Glu Glu Leu Lys 485 Lys Pro Glu Glu Asp Phe 490 Asp Ser His Gly Asp 495 Ala
 Gly Gly Lys Trp 500 Lys Thr Val Ser Ser 505 Gly Leu Pro Glu Asp 510 Pro Glu
 Lys Ala Gly 515 Gln Lys Ala Ser Leu 520 Ser Val Ser Gln Thr 525 Gly Ser Trp
 Arg Arg 530 Gly Met Ser Ala Gln 535 Gly Gly Ala Pro Ser 540 Arg Gln Lys Ala
 Gly Thr 545 Ser Ala Leu Lys 550 Thr Pro Gly Lys Thr 555 Asp Asp Ala Lys Ala 560
 Ser Glu Lys Gly Lys 565 Ala Pro Leu Lys Gly 570 Ser Ser Leu Gln Arg Ser 575
 Pro Ser Asp Ala 580 Gly Lys Ser Ser Gly 585 Asp Glu Gly Lys Lys 590 Pro Pro
 Ser Gly Ile 595 Gly Arg Ser Thr Ala 600 Thr Ser Ser Phe Gly 605 Phe Lys Lys
 Pro Ser 610 Gly Val Gly Ser Ser 615 Ala Met Ile Thr Ser 620 Ser Gly Ala Thr
 Ile Thr 625 Ser Gly Ser Ala Thr Leu Gly Lys Ile 635 Pro Lys Ser Ala Ala 640
 Ile Gly Gly Lys Ser 645 Asn Ala Gly Arg Lys 650 Thr Ser Leu Asp Gly 655 Ser
 Gln Asn Gln Asp Asp Val Val Leu His Val Ser Ser Lys Thr Thr Leu

Corrected Sequence Listing2.ST25

660

665

670

Gln Tyr Arg Ser Leu Pro Arg Pro Ser Lys Ser Ser Thr Ser Gly Ile
675 680 685

Pro Gly Arg Gly Gly His Arg Ser Ser Thr Ser Ser Ile Asp Ser Asn
690 695 700

Val Ser Ser Lys Ser Ala Gly Ala Thr Thr Ser Lys Leu Arg Glu Pro
705 710 715 720

Thr Lys Ile Gly Ser Gly Arg Ser Ser Pro Val Thr Val Asn Gln Thr
725 730 735

Asp Lys Glu Lys Glu Lys Val Ala Val Ser Asp Ser Glu Ser Val Ser
740 745 750

Leu Ser Gly Ser Pro Lys Ser Ser Pro Thr Ser Ala Ser Ala Cys Gly
755 760 765

Ala Gln Gly Leu Arg Gln Pro Gly Ser Lys Tyr Pro Asp Ile Ala Ser
770 775 780

Pro Thr Phe Arg Arg Leu Phe Gly Ala Lys Ala Gly Gly Lys Ser Ala
785 790 795 800

Ser Ala Pro Asn Thr Glu Gly Val Lys Ser Ser Ser Val Met Pro Ser
805 810 815

Pro Ser Thr Thr Leu Ala Arg Gln Gly Ser Leu Glu Ser Pro Ser Ser
820 825 830

Gly Thr Gly Ser Met Gly Ser Ala Gly Gly Leu Ser Gly Ser Ser Ser
835 840 845

Pro Leu Phe Asn Lys Pro Ser Asp Leu Thr Thr Asp Val Ile Ser Leu
850 855 860

Ser His Ser Leu Ala Ser Ser Pro Ala Ser Val His Ser Phe Thr Ser
865 870 875 880

Gly Gly Leu Val Trp Ala Ala Asn Met Ser Ser Ser Ser Ala Gly Ser
885 890 895

Lys Asp Thr Pro Ser Tyr Gln Ser Met Thr Ser Leu His Thr Ser Ser
900 905 910

Corrected Sequence Listing2.ST25

Glu Ser Ile Asp Leu Pro Leu Ser His His Gly Ser Leu Ser Gly Leu
915 920 925

Thr Thr Gly Thr His Glu Val Gln Ser Leu Leu Met Arg Thr Gly Ser
930 935 940

Val Arg Ser Thr Leu Ser Glu Ser Met Gln Leu Asp Arg Asn Thr Leu
945 950 955 960

Pro Lys Lys Gly Leu Arg Tyr Thr Pro Ser Ser Arg Gln Ala Asn Gln
965 970 975

Glu Glu Gly Lys Glu Trp Leu Arg Ser His Ser Thr Gly Gly Leu Gln
980 985 990

Asp Thr Gly Asn Gln Ser Pro Leu Val Ser Pro Ser Ala Met Ser Ser
995 1000 1005

Ser Ala Ala Gly Lys Tyr His Phe Ser Asn Leu Val Ser Pro Thr
1010 1015 1020

Asn Leu Ser Gln Phe Asn Leu Pro Gly Pro Ser Met Met Arg Ser
1025 1030 1035

Asn Ser Ile Pro Ala Gln Asp Ser Ser Phe Asp Leu Tyr Asp Asp
1040 1045 1050

Ser Gln Leu Cys Gly Ser Ala Thr Ser Leu Glu Glu Arg Pro Arg
1055 1060 1065

Ala Ile Ser His Ser Gly Ser Phe Arg Asp Ser Met Glu Glu Val
1070 1075 1080

His Gly Ser Ser Leu Ser Leu Val Ser Ser Thr Ser Ser Leu Tyr
1085 1090 1095

Ser Thr Ala Glu Glu Lys Ala His Ser Glu Gln Ile His Lys Leu
1100 1105 1110

Arg Arg Glu Leu Val Ala Ser Gln Glu Lys Val Ala Thr Leu Thr
1115 1120 1125

Ser Gln Leu Ser Ala Asn Ala His Leu Val Ala Ala Phe Glu Lys
1130 1135 1140

Ser Leu Gly Asn Met Thr Gly Arg Leu Gln Ser Leu Thr Met Thr
1145 1150 1155

Corrected Sequence Listing2.ST25

Ala	Glu	Gln	Lys	Glu	Ser	Glu	Leu	Ile	Glu	Leu	Arg	Glu	Thr	Ile
	1160					1165					1170			
Glu	Met	Leu	Lys	Ala	Gln	Asn	Ser	Ala	Ala	Gln	Ala	Ala	Ile	Gln
	1175					1180					1185			
Gly	Ala	Leu	Asn	Gly	Pro	Asp	His	Pro	Pro	Lys	Asp	Leu	Arg	Ile
	1190					1195					1200			
Arg	Arg	Gln	His	Ser	Ser	Glu	Ser	Val	Ser	Ser	Ile	Asn	Ser	Ala
	1205					1210					1215			
Thr	Ser	His	Ser	Ser	Ile	Gly	Ser	Gly	Asn	Asp	Ala	Asp	Ser	Lys
	1220					1225					1230			
Lys	Lys	Lys	Lys	Lys	Asn	Trp	Leu	Arg	Ser	Ser	Phe	Lys	Gln	Ala
	1235					1240					1245			
Phe	Gly	Lys	Lys	Lys	Ser	Thr	Lys	Pro	Pro	Ser	Ser	His	Ser	Asp
	1250					1255					1260			
Ile	Glu	Glu	Leu	Thr	Asp	Ser	Ser	Leu	Pro	Ala	Ser	Pro	Lys	Leu
	1265					1270					1275			
Pro	His	Asn	Ala	Gly	Asp	Cys	Gly	Ser	Ala	Ser	Met	Lys	Pro	Ser
	1280					1285					1290			
Gln	Ser	Ala	Ser	Ala	Ile	Cys	Glu	Cys	Thr	Glu	Ala	Glu	Ala	Glu
	1295					1300					1305			
Ile	Ile	Leu	Gln	Leu	Lys	Ser	Glu	Leu	Arg	Glu	Lys	Glu	Leu	Lys
	1310					1315					1320			
Leu	Thr	Asp	Ile	Arg	Leu	Glu	Ala	Leu	Ser	Ser	Ala	His	His	Leu
	1325					1330					1335			
Asp	Gln	Ile	Arg	Glu	Ala	Met	Asn	Arg	Met	Gln	Asn	Glu	Ile	Glu
	1340					1345					1350			
Ile	Leu	Lys	Ala	Glu	Asn	Asp	Arg	Leu	Lys	Ala	Glu	Thr	Gly	Asn
	1355					1360					1365			
Thr	Ala	Lys	Pro	Thr	Arg	Pro	Pro	Ser	Glu	Ser	Ser	Ser	Ser	Thr
	1370					1375					1380			
Ser	Ser	Ser	Ser	Ser	Arg	Gln	Ser	Leu	Gly	Leu	Ser	Leu	Asn	Asn
	1385					1390					1395			

Corrected Sequence Listing2.ST25

Leu	Asn	Ile	Thr	Glu	Ala	Val	Ser	Ser	Asp	Ile	Leu	Leu	Asp	Asp
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Ala	Gly	Asp	Ala	Thr	Gly	His	Lys	Asp	Gly	Arg	Ser	Val	Lys	Ile
	1415					1420					1425			
Ile	Val	Ser	Ile	Ser	Lys	Gly	Tyr	Gly	Arg	Ala	Lys	Asp	Gln	Lys
	1430					1435					1440			
Ser	Gln	Ala	Tyr	Leu	Ile	Gly	Ser	Ile	Gly	Val	Ser	Gly	Lys	Thr
	1445					1450					1455			
Lys	Trp	Asp	Val	Leu	Asp	Gly	Val	Ile	Arg	Arg	Leu	Phe	Lys	Glu
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Tyr	Val	Phe	Arg	Ile	Asp	Thr	Ser	Thr	Ser	Leu	Gly	Leu	Ser	Ser
	1475					1480					1485			
Asp	Cys	Ile	Ala	Ser	Tyr	Cys	Ile	Gly	Asp	Leu	Ile	Arg	Ser	His
	1490					1495					1500			
Asn	Leu	Glu	Val	Pro	Glu	Leu	Leu	Pro	Cys	Gly	Tyr	Leu	Val	Gly
	1505					1510					1515			
Asp	Asn	Asn	Ile	Ile	Thr	Val	Asn	Leu	Lys	Gly	Val	Glu	Glu	Asn
	1520					1525					1530			
Ser	Leu	Asp	Ser	Phe	Val	Phe	Asp	Thr	Leu	Ile	Pro	Lys	Pro	Ile
	1535					1540					1545			
Thr	Gln	Arg	Tyr	Phe	Asn	Leu	Leu	Met	Glu	His	His	Arg	Ile	Ile
	1550					1555					1560			
Leu	Ser	Gly	Pro	Ser	Gly	Thr	Gly	Lys	Thr	Tyr	Leu	Ala	Asn	Lys
	1565					1570					1575			
Leu	Ala	Glu	Tyr	Val	Ile	Thr	Lys	Ser	Gly	Arg	Lys	Lys	Thr	Glu
	1580					1585					1590			
Asp	Ala	Ile	Ala	Thr	Phe	Asn	Val	Asp	His	Lys	Ser	Ser	Lys	Glu
	1595					1600					1605			
Leu	Gln	Gln	Tyr	Leu	Ala	Asn	Leu	Ala	Glu	Gln	Cys	Ser	Ala	Asp
	1610					1615					1620			
Asn	Asn	Gly	Val	Glu	Leu	Pro	Val	Val	Ile	Ile	Leu	Asp	Asn	Leu

Corrected Sequence Listing2.ST25
1630 1635

1625	His	His	Val	Gly	Ser	Leu	Ser	Asp	Ile	Phe	Asn	Gly	Phe	Leu	Asn
	1640						1645					1650			
	Cys	Lys	Tyr	Asn	Lys	Cys	Pro	Tyr	Ile	Ile	Gly	Thr	Met	Asn	Gln
	1655						1660					1665			
	Gly	Val	Ser	Ser	Ser	Pro	Asn	Leu	Glu	Leu	His	His	Asn	Phe	Arg
	1670						1675					1680			
	Trp	Val	Leu	Cys	Ala	Asn	His	Thr	Glu	Pro	Val	Lys	Gly	Phe	Leu
	1685						1690					1695			
	Gly	Arg	Tyr	Leu	Arg	Arg	Lys	Leu	Ile	Glu	Ile	Glu	Ile	Glu	Arg
	1700						1705					1710			
	Asn	Ile	Arg	Asn	Asn	Asp	Leu	Val	Lys	Ile	Ile	Asp	Trp	Ile	Pro
	1715						1720					1725			
	Lys	Thr	Trp	His	His	Leu	Asn	Ser	Phe	Leu	Glu	Thr	His	Ser	Ser
	1730						1735					1740			
	Ser	Asp	Val	Thr	Ile	Gly	Pro	Arg	Leu	Phe	Leu	Pro	Cys	Pro	Met
	1745						1750					1755			
	Asp	Val	Glu	Gly	Ser	Arg	Val	Trp	Phe	Met	Asp	Leu	Trp	Asn	Tyr
	1760						1765					1770			
	Ser	Leu	Val	Pro	Tyr	Ile	Leu	Glu	Ala	Val	Arg	Glu	Gly	Leu	Gln
	1775						1780					1785			
	Met	Tyr	Gly	Lys	Arg	Thr	Pro	Trp	Glu	Asp	Pro	Ser	Lys	Trp	Val
	1790						1795					1800			
	Leu	Asp	Thr	Tyr	Pro	Trp	Ser	Ser	Ala	Thr	Leu	Pro	Gln	Glu	Ser
	1805						1810					1815			
	Pro	Ala	Leu	Leu	Gln	Leu	Arg	Pro	Glu	Asp	Val	Gly	Tyr	Glu	Ser
	1820						1825					1830			
	Cys	Thr	Ser	Thr	Lys	Glu	Ala	Thr	Thr	Ser	Lys	His	Ile	Pro	Gln
	1835						1840					1845			
	Thr	Asp	Thr	Glu	Gly	Asp	Pro	Leu	Met	Asn	Met	Leu	Met	Lys	Leu
	1850						1855					1860			

Corrected Sequence Listing2.ST25
 Gln Glu Ala Ala Asn Tyr Ser Ser Thr Gln Ser Cys Asp Ser Glu
 1865 1870 1875

Ser Thr Ser His His Glu Asp Ile Leu Asp Ser Ser Leu Glu Ser
 1880 1885 1890

Thr Leu
 1895

<210> 13
 <211> 3682
 <212> DNA
 <213> Homo sapiens

<400> 13
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 gaactgaggg gcaggtgtga gggatgaagc aggagtaggt aggggctaga tcacaaaaga 180
 tctatgccag tgtttctcac agtgtgattc ccagcccagt agcatgatat cacttgggat 240
 cttgttagaa atacaaattc ttatacatca ccctggacta gaccacctga ataagaaaag 300
 ttgggcatga ggcctacaaa tttttaaaaa agtcatacag gtgattgcaa tgcattgctaa 360
 agtttgagaa acactctttg ctgtgggttg aatatttgtg tccttccaaa attcatgtag 420
 aaaccatctc caatgttata gtattaagag gagggaccct tgggagctga tcagatcatg 480
 aagtctcctt tcttataaag gggattaaaa gccttggccc ttttaccctt tgtccatgta 540
 aggacacagt gttggaagca gggactgggt tctcaccaga aacagaacct gccagcctct 600
 tgggtcttga cttctcagcc tccacaattg tgagaaataa gtttctgttg tttataagtt 660
 aaccagtctc aggtattttg taatggcagc acaaaggggc taagaaactg ttctatgccc 720
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 ggaagcgtgg tggaggtgag aggactggag gttaagttgg tagggagata caggaaagaa 900
 gcttatgaca cttgagttaa aatgtagcat ccttcctatg tgtagggctc ataaaaatgt 960
 atagtctaag atagaacaca gaatactcta tgaatcctgc ccacaagggtg ttggtaatct 1020
 agattcactt ttttttctg ataatgccat ccatatgtat ggagcgtcta ctactgtatg 1080
 ccagagtga cttggaatcg gtttggttga tctagacaag accataagga ggtccccctt 1140
 actacctctt ctccagggga gggattcaag ttgaactagt acttcagaga ctgttttagta 1200
 atatcatgca tgaaagggtga tgggttaggac agaaaaataa atggattgca tcataattcc 1260
 tcaggttctc caaatatgtg gtggtctcaa accatgtgaa ttggtctgca catcctgttt 1320
 gggttgcgtg tcagcagttg agatctgagc cttatttcta acagtgaac agtgagagac 1380

Corrected Sequence Listing2.ST25

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aaaggtgccg gtaggcgggc aggtgagcct gtggataatc ctggagtaaa ggttcaatag	1560
accttcaagt ctatcctaca ggattcggag tgaggggaga gaaaaggaga cgcttctctg	1620
gctgagagag gaagagaaaa aaaaatccca gatatctgac agctatatct tcccatcacc	1680
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ccccaccccc agcccatccc ccgtttgtag gtgtgctttc aatgaaaata agtcggtgtt	1800
catggacgga aactagagca gctgaaaata gatgcaagac ttgttgagca tacaatcat	1860
ttccccctta gtctccaagg gaggaaaaaa aatccctctt actctccttg cagcctgtgt	1920
tctgcattct ggagaggaag ctgaggctgg tcctcaggcg ctccctccgc cgttcccgca	1980
ggaaactttt ctcgcagggc ccgctccgtc catcccgcg cggtccaaga cggtaggcct	2040
cccgtgggct cctctcctgg gcaagggcc agaccccgcg acgcgcctgt ctctttaaat	2100
tccagctgcg cggctgggaa acagcgccac tcgccgccca ggccggctgg aggctgaaga	2160
gcgagctcgc gctttcgctc ccggctgcgc gccgcggaga gctgggctcg gcccgcgggc	2220
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ctccccgcc ccctccctt ctttattttt ttcctcttcg ctgcactctt ctcggctttt	2760
ccctgacac tactgatggg ggtgcggggg gacgtcgggg atgggggtgg ccagcgcggt	2820
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gagcgtccat acatcatagc tctccttccc actccccgc ccctcttcgg gattctctct	3060
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gggaatcggt tgtaaccctt tcgttctacc aacgtggaat agctgtgaaa cctgcagcgt	3240

Corrected Sequence Listing2.ST25

ggtcacctca gcctggctcgt tttcagaccc gtcctcatcc atcaacatat ttgtttcccg	3300
agtctattga tctccctgaa ttctacagaa atgcattcta agctaggcgc ctgtatgtca	3360
gaatcagttc tgcaggtagc ttccgtgctc caagtatgac atgtattgta agggctgcat	3420
ctgttttaaa cccacataag ccatgggtat aaataaatgt agctttgaaa aaaaatctgg	3480
ccttattcta gataaacttc cctcttaaata tactgatata ctcttctccc tctttgacat	3540
ttaatttttag gaaagttggg agacagggtc ttgtcctcca gtttttaagg agcaggcaac	3600
ttctattatc ttaattttct cgtctttgaa catcactcac gtttgacta cccagtcagt	3660
ggaacgagtg ggtcataatt aa	3682

<210> 14
 <211> 3904
 <212> DNA
 <213> Homo sapiens

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ctgacacatt tacaagatgc ttttggcagg ttggctggaa tttgaaggca catttaattg	120
taggtgcaat aaaatattca ttttctcttg ttcttgggtt gagatgtcat gcccttttgg	180
tcacttatat tttgggtgtga ctgtgtgtgt gtgtgtatgt gtttgtgtga aggatttaac	240
aaagtctgtt ctaactgtca tgtgatttga agttaaaagg tatgttagtg acaagccaca	300
aatttctctt atttatagta cattgatcct gaaaccattt tttcccttgt gatttcttct	360
gtgcatggat catttaacga aagggtggca atgatgagct atttttttat aataggaaaa	420
aaattcctca agtttactta ccaagtcata tttttatata gagggattag caaatatttc	480
tgatctaata ttttaataga ctgaattgct gaccactgct aattaccaag aatataattt	540
cttaattctg aaattgctgt acctctcaag ttgtctggag gactccaagt gacccaactt	600
gtaactcatg gcaacaggaa gtggttgttc tgggtgcaag ctgaagtgtg cacatggacc	660
cgtactttgt tagcactcgg ggacttgata tggaaagaat taatgtactg gcttttttgt	720
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cttgaaaact gcaactttaa gcaaaaggaa gtataatgaa acacttttat cacaggctaa	900
ttggtagaaa caagacttaa gttcccatgg catatttctg gtcacaaaaa catttccaaa	960
cttctcaaaa cacttcaata ttaagcattc aaatacatgt aaactatgta tatatgtaag	1020
aaaggttact ataaaccaga tcaatattta cccaattatt taagttcagg gtcttaggtg	1080
gctggagcct atccgagtag ctgagggcac aaggcgggaa ccagccctag acaggacacc	1140
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Corrected Sequence Listing2.ST25

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tccatacaga tatggggaga atgtacaaac tccaccaga cagtggaccc agccaggaat	1320
caacatttgg gcaacattat aatgaaacga agttgaatga aatgatgtcg ttccacgacc	1380
tgtgtacttt gaggggtgtt ataaaattct cagaagacag aggtttaatg ctatcttttt	1440
aatagaaaat aacttataga gaagtgtgca catgtgactt tgtgtgtagc aggaatcatt	1500
aggatgagaa tcagacgtaa gaggtggtgc caacatgagg aatgttgaga ttcaggaggc	1560
tgtggatgga agtagaagcc agaaggccag ggtaggttc ctacttctta ctgtttcagt	1620
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agagggtcac atatgtagca gtaatggata ctaaatgata cactcggagg aaacagaaaa	1800
gacttctgaa tagagactgg agatacttcc ttggaccatt gatgaatggg caatgatgca	1860
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gaaaaatccc cagagctatc tttctgcaca gacttcattt tttctcccaa gtctgactgt	2160
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tcagataatc aggacctaga gacttcaaga tctggaagca ttgctggtga catagagcaa	2580
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aaaatcatat tttttgggaa tttattcccc cgatcaaaag aagcatttgt tattgaacac	2940
agtcttatgc taccttatta agatgtatca aacaccctga ttgatcaaaa acacctcagt	3000
ccatttttaag gcagtattgc ccagcaatta aagatgtagc ttctggagga gtctttctga	3060
gtttgaattc agtactcttc cacgtactat atagggtgatc ttgggtaaac ttcttgagtc	3120

Corrected Sequence Listing2.ST25

tcagtatccc catctgtaaa attgtttag agagaattt ttgtgatgat taggtgagag	3180
aatatattaa tgtaatatatt aggagagcaa ccagcatgta gcatatatc attacatatc	3240
aatttctata ttattgatgt tcatactgct gatgttgaaa tgcacaggaa ggccacagtt	3300
atthttctgtt tagattgatt tttcttttaa agtctgaaca taaactgtaa tactgtgctt	3360
atthtatgtag gaactgtgat ctctgtctct ctttttccca tctccccctc tctaccttag	3420
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aagctatgag gatacaaagg cataagaatg acacaacaga ctttggagac ttggggaaag	3660
ggtgggaagg ggggtgagga taaaagacta caaatagggt gcagtgtata ctgcttggtt	3720
ggtgggtgca ccaaatctc acaaatcacc accaaagaac ttactcatgt aaccaaacac	3780
cacctgttcc ccagtaacct atggatataa aaaaattaaa aaaaagaaaa aaagaaaact	3840
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gctt	3904

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 <212> DNA
 <213> Homo sapiens

<400> 15	
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gtttgttaca tcattatgac acaagtcaa catgagtctt gtgaattgca tgctaaatct	180
aatattttgag cagcgtaca actttggggt tagagatgtt atcagtggag tttctttatg	240
tttcctaact gtccccctct gactgccagc tttcttatct gaagaacatt ttaaacaat	300
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aatcacaaaa tcaaggacat taaatgaaag tgtctgttaa aggcatatta taaatgaatc	720
ataagccaca cagttctctg tgatgtacga agtgggcatt taaagagggt ctgatttgat	780
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Corrected Sequence Listing2.5T25

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ttgggctcta catggaaaaa cacatgaaat taaaaagtgg cacaaatgtt tagttagtag	1020
aacatctggc taattgggat caaataattc aaccatgtgg gaacgttttt gctcaaaata	1080
gataatttg tgaattgtttca tataggcaaa tgattagaca acttcctctt cctcaaagt	1140
gaacggacag atgtgatcta gaagcaagac actcttttgt gtaaatattc cctttggcct	1200
aaagcaaaag tggacagact ttaaaccact gagagcagag cagtgtgtgt taagattgca	1260
atatcttaag ctcttgagtt aaatggaaaa tgaaaaacaa aagtgtatat ttggaagtta	1320
ggaatgtttt ctttaaaata taaaataaaa ttttagattt aagatcacia gaaatattac	1380
tgaagactta tactcttcct ggggctaagg gaggtgacag tcgctcatca gaaaaaaaaa	1440
aatgccctca tttcctaact tttctaaaaa atataatata agttcaggct aatacttcct	1500
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gactaccaa gtgtccaatt aagcaacacg ataccaccgt tattgatatt ctagcaagaa	1620
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atcttcttag acaagagttt tcatacgata taataaagac atctggaatt tgtcttgat	1980
gcaatatgaa atttgctatt aaacgtggag ttaaaacttt atgtcaatag atccaataac	2040
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 <211> 2103
 <212> DNA
 <213> Homo sapiens

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agtttgcata tataacttgg gtgtgaccaa gcaagggtgag agttaagaac ttttaaaact	180
tactgtatta tattgataga actcagaaaag tactaacttg aatattatta ttctaattgc	240
ttttcccttt tagttattaa aaataagaat acttaaatta ataacaagat cttttactgg	300
caggattaac caaattatct gtaatgtgtt cctcgaatgc ttttaagtgg aaatatactt	360

Corrected Sequence Listing2.ST25

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aaaacaaatt gttgaaagta cagtggcttt tcatatgtat gatttgtaaa acaaattagc	540
ttttttaaag tgatgtgacg cttaatgaga agaaatcagt agagaattac aaactgcact	600
tcaaaaagata catctaatat cattttaata atgaaatttg aaaaaatagt gtgctcgttt	660
tacagtctca ttaaatgaat taaaatatca gcacacattg tagtaggtta tcattggcag	720
agaaggctga aatagaaacg ttacaatggg atgcactgcc atctgaacat tatgtcgaag	780
tggaacgcgg aaacatatatt ctcagaacaa gtggtaaaat gaaaacagca tcatttgtaa	840
agcatttctt ttgagagtgc ttcagtttct tctcctgatg acctgccatt cagaaactga	900
caatgaataa tacactctga caccagcatt tgtcaatttg cccagaacca tatgagagta	960
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taagatagat gccaaaggatt tagcaacatt ttaattcaac attatacagg tatcagagtt	1500
aatgagaatt atgcattagt ctttaaattt gggcagctta ttcagctaaa acatagatgt	1560
ctagctctta aacactttgt ttttttaatt actctgaaat tacaataaag tcaaagaact	1620
gaactgtttt cttttcaagc cagtgc aaat gtgctttagt tattatttta ctggtgatct	1680
aattatgcat tttaatgctt tattacttaa tacttatata agcctaaaat acgttggtta	1740
tgtcataatt tcagggattt tagtattctt tccatgagtt accataacta ggtgcatatg	1800
tgtaaatata cgtatatatc tatatctata tatttatatc tatgtatata tcaatttata	1860
agactaaata gacttgcca tatgtgttgt tggtttatgc atacatgcac aaatattgag	1920
gtgtccacaa agtatatatg cctgtacata aattacatac tggctggtga gtgaatgtaa	1980
gcttctctaa attgtacaac tctccacaga gtggcactct aatattgcaa aggtacaata	2040
taagcatgtg cagaatgaac agctcttcta ggatccctat aaaactccac cccatgtttc	2100
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Corrected Sequence Listing2.ST25

<211> 4260
<212> DNA
<213> Homo sapiens

<400> 17
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tgaggaggct gtctgtccct tagcggagct agaacactgt gctcggagat ccgctgctct 180
cttcagagct ggcaggcaag agtgtttttag tctgctgagc ctgcgcccac agccgcccct 240
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tgctaccttt ctttcagata tgccccgccc agagaggagg aatctagaga ggcagtctgg 360
ctacagcagc tttgccaagc tgcagtgggc tctgcccagt ccaaaattcc cagcgggttt 420
gtttacattg tgaggggaaa agcacctact caagcctcag ttatggcagt tgccccctcc 480
cccaccaagc tccagggtcc caggtgtcct tcagactgct gtgctggcaa tgagaatttc 540
aagccagtgg atcttagctt gctgggctcc acaggggtgg gatccactga gctagaccac 600
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ccaggtgcta ctgggggatg aaaaaaaaaa ctctgcagc tagcttggtg tctgcccagt 720
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atgtgtgaa gactgtggga aaagcatagt atctgggctg gatagctccg tccttcaagg 840
cacagtccct catgacttcc cttggctagg ggagggagtt cccaaccct ttgcacttcc 900
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caagtgattt ttttttattt taaggTcaaa tctacaaaat attatagtgt tatcaccact 1200
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caaatttatc atattgcttt cctaggtgaa gaccctgaaa caagaagaat gagaacagtt 1440
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cagataagcc acaggttttt ttcaattttg catatatattg agccaataaa gaaaaaataa 1560
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ctattttctc ccttgtttta tatcaaattg attggttaatt atccttaaac tgagaattca 1680
cagtatatac ctatttatct tttatctcta tctctatctg ctatttatgt ctttttcagt 1740

Corrected Sequence Listing2.ST25

ataattttcca	gtactgcaac	taccaccatc	actgtttaagt	ggattttgtaa	tacctgtcct	1800
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caaacataat	tgtagttaac	tttcagaata	ggctctgggaa	ggttacagtg	agttaaggat	1920
ttgttgaaaa	tgtaaaacaa	tatgtttgtt	tacccaaggt	gtactgatgg	cctttctttt	1980
gaaaacaaac	gaaaagctat	aaaatgtatg	cccctttcca	caatttgacc	tcaaaatgaa	2040
tatagagttt	agcttttcggg	aagatgacgt	gtttataaga	gatgaccctc	aactccagcc	2100
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ccatttttatt	tgacagcacc	ctggagacaa	catttgacag	cactgtgaca	acagaagtta	2220
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aggcatgtcc	gcgacttcag	gcgggagatg	ctccctccct	gggtgctggc	tatcctcgca	2340
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gtcgagctgc	tgtctctagg	ctgggaaaca	tgtcacagat	tgacatgagt	gagaaagcaa	2460
gcagtgacct	ggacatgtct	tctgaggctg	atgtgggttg	atatatgagt	gatggtgata	2520
tccttgggaa	aagtctcagg	actgatgaca	tcaacagtgg	gtaagtaacc	ctgttctccg	2580
tcagcattgt	gtgaagaggg	gaggtggtct	actataatgc	attcactata	aacaaatgtg	2640
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ataagccgct	aagtttttct	gttggtgaga	gaaacacatg	tggcttctgt	ttttcagagt	2820
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gaataggtcc	aaaaggaggc	aataggatat	tctattaata	attgtaattg	ccatttttag	3240
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Corrected Sequence Listing2.ST25

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tgtggacccc ttcggaacct aacgtatcca aattagtttt tgtcatctag aataaggata	3900
aaattgtacc atcttcatga agttgtagg atcatccaca aatttttagtt tgcgcaatgc	3960
ttggcatgat acaagcactc aataaattta tcatcttcct ctttatcatc actattacat	4020
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tatgtattta acatagccta ggaggcaatg ccagttcag aaaacataat ggcaaagcaa	4140
gagtgtctaa ggcacactct ttctcccatc tctctcttct ttcttctcca ttctttccac	4200
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<210> 18
 <211> 2429
 <212> DNA
 <213> Homo sapiens

<400> 18	
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ttgtggagtg aatgaacaaa ttaatgaata taggctatit attaatagg caatatagtc	180
acataggctg gcaatcgcac ctaattaaat agagtggtaa atgagttcca gaaagaacta	240
aggatctaca aggatgttat gaaagagaaa aatgagttat gtgaaaaata ggagacagt	300
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attattgtta gctgaaagta gaaaacgtca tgggagggaa tatctgctag tttttggtaa	420
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gggataatca actctccttg ctccatcagg gccccagact gggctctggc agaggaactc	540
agaacaacgt aaagacctag ataggatatc aataaattgg gacctgtgaa aacagtgcc	600
cttaagtgt ggtacctgga ccagcagcag cagcagcagc agccattgaa acttcataga	660
aagacagatt ctgagcttca tccaagactt actgaattag aatatctcaa ggtaaggcct	720
ggtaattctga gctttaacta gccctcaagg tgattcttaa gttcaagcat cactatatta	780
agttgaacaa atagatgccg ggcctataaa tacatgtaac gcctagcata aatatttcaa	840
cattaaaaat gacatttcat agttcttatt taccctatta gctgtgttct gtcaagataa	900
tgagaatatt gatatgttag aatacactga tgcactaatt tttaaattag atcaaataat	960
gacttggtat acctgaaata aattggttca gcttggtaga tgcagttttt gagaattata	1020
taagtcattt ttaaaagaat aattttaact tgagctgctt gcataaatta aattgcaaaa	1080

Corrected Sequence Listing2.ST25

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aaggattcag gtcttttact tcctattttg tgggtcccaa ctacttttgc caaaggcttt 2340
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<210> 19
 <211> 2926
 <212> DNA
 <213> Mouse

<220>
 <221> CDS
 <222> (2)..(2926)
 <223>

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<400> 19
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  Ser His Ser Thr Leu Glu Thr Thr Phe Asp Thr Thr Val Thr Thr Glu
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Corrected Sequence Listing2.ST25																
gtg	aat	gga	agg	gcc	atc	ccc	aac	ctg	aca	agc	cga	cct	tcc	ccc	atg	97
Val	Asn	Gly	Arg	Ala	Ile	Pro	Asn	Leu	Thr	Ser	Arg	Pro	Ser	Pro	Met	
			20					25					30			
acc	tgg	aga	ctg	ggt	caa	gcg	tgc	cct	cgt	cta	cag	gct	gga	gat	gcc	145
Thr	Trp	Arg	Leu	Gly	Gln	Ala	Cys	Pro	Arg	Leu	Gln	Ala	Gly	Asp	Ala	
			35				40					45				
ccc	tcc	atg	ggc	gct	gga	tat	tct	cga	agc	ggt	acc	agc	cga	ttc	atc	193
Pro	Ser	Met	Gly	Ala	Gly	Tyr	Ser	Arg	Ser	Gly	Thr	Ser	Arg	Phe	Ile	
		50				55					60					
cac	acg	gat	ccc	tcc	agg	ttt	atg	tat	acc	acg	cct	ctc	cgc	cga	gct	241
His	Thr	Asp	Pro	Ser	Arg	Phe	Met	Tyr	Thr	Thr	Pro	Leu	Arg	Arg	Ala	
					70					75					80	
gct	gtc	tcg	cgt	ctg	gga	aac	atg	tca	caa	ata	gat	atg	agc	gag	aaa	289
Ala	Val	Ser	Arg	Leu	Gly	Asn	Met	Ser	Gln	Ile	Asp	Met	Ser	Glu	Lys	
				85					90					95		
gca	agc	agt	gac	ctg	gat	gtg	tct	tct	gaa	gtg	gat	gtt	ggt	gga	tac	337
Ala	Ser	Ser	Asp	Leu	Asp	Val	Ser	Ser	Glu	Val	Asp	Val	Gly	Gly	Tyr	
			100					105					110			
atg	agc	gat	ggt	gat	atc	ctt	ggg	aag	agt	ctg	aga	gcg	gat	gat	atc	385
Met	Ser	Asp	Gly	Asp	Ile	Leu	Gly	Lys	Ser	Leu	Arg	Ala	Asp	Asp	Ile	
		115					120					125				
aac	agt	ggg	tac	atg	aca	gat	ggt	ggg	ctc	aac	cta	tat	acc	aga	agt	433
Asn	Ser	Gly	Tyr	Met	Thr	Asp	Gly	Gly	Leu	Asn	Leu	Tyr	Thr	Arg	Ser	
		130				135					140					
ctt	aac	cga	gtc	ccg	gac	aca	gca	act	tcc	aga	gat	gtc	ata	cag	aga	481
Leu	Asn	Arg	Val	Pro	Asp	Thr	Ala	Thr	Ser	Arg	Asp	Val	Ile	Gln	Arg	
					150					155					160	
ggc	gtt	cac	gat	gtg	aca	gtg	gac	gca	gac	agc	tgg	gat	gac	agc	agt	529
Gly	Val	His	Asp	Val	Thr	Val	Asp	Ala	Asp	Ser	Trp	Asp	Asp	Ser	Ser	
				165					170					175		
tct	gtg	agc	agt	ggc	ctc	agt	gac	aca	ctt	gat	aac	att	agc	aca	gat	577
Ser	Val	Ser	Ser	Gly	Leu	Ser	Asp	Thr	Leu	Asp	Asn	Ile	Ser	Thr	Asp	
			180					185					190			
gac	ctc	aac	acc	acg	tcc	tcc	atc	agt	tct	tac	tcc	aac	atc	act	gtc	625
Asp	Leu	Asn	Thr	Thr	Ser	Ser	Ile	Ser	Ser	Tyr	Ser	Asn	Ile	Thr	Val	
			195				200					205				
ccc	tcc	agg	aag	aac	act	cag	ctg	aaa	aca	gat	gcg	gag	aaa	cgt	tcg	673
Pro	Ser	Arg	Lys	Asn	Thr	Gln	Leu	Lys	Thr	Asp	Ala	Glu	Lys	Arg	Ser	
		210				215					220					
aca	aca	gat	gag	acc	tgg	gat	agt	cct	gag	gag	ctg	aag	aaa	gcc	gag	721
Thr	Thr	Asp	Glu	Thr	Trp	Asp	Ser	Pro	Glu	Glu	Leu	Lys	Lys	Ala	Glu	
					230					235					240	
gga	gat	tgt	gac	agc	cat	ggt	gac	gga	gcc	gcc	aag	tgg	aag	ggt	gct	769
Gly	Asp	Cys	Asp	Ser	His	Gly	Asp	Gly	Ala	Ala	Lys	Trp	Lys	Gly	Ala	
				245					250					255		
act	tct	gga	ctt	gct	gaa	gac	tcg	gag	aag	aca	ggg	cag	aaa	gcc	agc	817
Thr	Ser	Gly	Leu	Ala	Glu	Asp	Ser	Glu	Lys	Thr	Gly	Gln	Lys	Ala	Ser	
			260					265					270			

Corrected Sequence Listing2.ST25

ctg tct gtg tct cag aca ggc tcc tgg agg aga ggc atg tct gcc cag	865
Leu Ser Val Ser Gln Thr Gly Ser Trp Arg Arg Gly Met Ser Ala Gln	
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	280
	285
gga gga act cca gct aca gct agg cag aaa acc agc aca agt gca ctc	913
Gly Gly Thr Pro Ala Thr Ala Arg Gln Lys Thr Ser Thr Ser Ala Leu	
	290
	295
	300
aag acc cct ggg aag aca gat gat gcc aaa gct tcc gag aaa ggg aaa	961
Lys Thr Pro Gly Lys Thr Asp Asp Ala Lys Ala Ser Glu Lys Gly Lys	
	305
	310
	315
	320
act cct ctc aaa gga tca tcc ttg caa agg tct cct tca gat gca ggg	1009
Thr Pro Leu Lys Gly Ser Ser Leu Gln Arg Ser Pro Ser Asp Ala Gly	
	325
	330
	335
aaa agc agc ggg gat gaa ggg aaa aag cca ccg tca ggc att gga aga	1057
Lys Ser Ser Gly Asp Glu Gly Lys Lys Pro Pro Ser Gly Ile Gly Arg	
	340
	345
	350
tcg aca gcc agc agt tct ttt gga tac aag aag cca agt ggt gta ggg	1105
Ser Thr Ala Ser Ser Ser Phe Gly Tyr Lys Lys Pro Ser Gly Val Gly	
	355
	360
	365
gct tcc act atg att acc agc agc ggt gcc acc atc aca agc ggt tca	1153
Ala Ser Thr Met Ile Thr Ser Ser Gly Ala Thr Ile Thr Ser Gly Ser	
	370
	375
	380
gct aca ctg ggg aaa atc ccc aaa tcc gct gcc att ggt ggg aag tcc	1201
Ala Thr Leu Gly Lys Ile Pro Lys Ser Ala Ala Ile Gly Gly Lys Ser	
	385
	390
	395
	400
aat gca gga agg aaa acc agc ctg gac ggg tcc cag aat caa gat gat	1249
Asn Ala Gly Arg Lys Thr Ser Leu Asp Gly Ser Gln Asn Gln Asp Asp	
	405
	410
	415
gtt gtc ctg cac gtg agc tcg aag acc acc ctc cag tac cgt agt ttg	1297
Val Val Leu His Val Ser Ser Lys Thr Thr Leu Gln Tyr Arg Ser Leu	
	420
	425
	430
ccc cgc cct tct aag tcc agc acc agc gga atc cct ggg aga ggt ggc	1345
Pro Arg Pro Ser Lys Ser Ser Thr Ser Gly Ile Pro Gly Arg Gly Gly	
	435
	440
	445
cac agg tcg agc acc agc agc att gat tcc aat gtc agc agc aag tca	1393
His Arg Ser Ser Thr Ser Ser Ile Asp Ser Asn Val Ser Ser Lys Ser	
	450
	455
	460
gct ggg gcc acc acc tcc aaa ctg aga gaa ccg act aag atc ggc tca	1441
Ala Gly Ala Thr Thr Ser Lys Leu Arg Glu Pro Thr Lys Ile Gly Ser	
	465
	470
	475
	480
ggg cgc tcg agt cca gtc act gtc aac caa aca gac aaa gag aag gag	1489
Gly Arg Ser Ser Pro Val Thr Val Asn Gln Thr Asp Lys Glu Lys Glu	
	485
	490
	495
aaa gta gca gtg tca gat tca gag agc gtt tcc ttg tca ggt tcc ccc	1537
Lys Val Ala Val Ser Asp Ser Glu Ser Val Ser Leu Ser Gly Ser Pro	
	500
	505
	510
aaa tcc agc ccc acc tct gcc agt gcc tgt ggg act caa ggg ctc aga	1585
Lys Ser Ser Pro Thr Ser Ala Ser Ala Cys Gly Thr Gln Gly Leu Arg	

Corrected Sequence Listing2.ST25

515	520	525	
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ttg ttc ggt gcc aag gca ggc ggc aaa tct gcc tcc gca cct aat act Leu Phe Gly Ala Lys Ala Gly Gly Lys Ser Ala Ser Ala Pro Asn Thr 545 550 555 560			1681
gag ggg gcg aag tcc tcc tca gta gtg ctc agc cct agt acc tct tta Glu Gly Ala Lys Ser Ser Ser Val Val Leu Ser Pro Ser Thr Ser Leu 565 570 575			1729
gcc cga caa ggc agt ctg gag tca ccg tcg tcc ggt acg gga agc atg Ala Arg Gln Gly Ser Leu Glu Ser Pro Ser Ser Gly Thr Gly Ser Met 580 585 590			1777
ggc agt gct ggt ggg ctg agt ggc agc agc agc cct ctc ttc aat aaa Gly Ser Ala Gly Gly Leu Ser Gly Ser Ser Ser Pro Leu Phe Asn Lys 595 600 605			1825
ccc tca gac cta act aca gat gtt ata agc tta agt cac tcc ttg gct Pro Ser Asp Leu Thr Thr Asp Val Ile Ser Leu Ser His Ser Leu Ala 610 615 620			1873
tcc agc cca gcg tcg gtt cac tct ttc aca tcc ggt ggg ctt gtg tgg Ser Ser Pro Ala Ser Val His Ser Phe Thr Ser Gly Gly Leu Val Trp 625 630 635 640			1921
gct gcc aat ctg agc agt tcc tct gcc ggc agc aag gac act cca agt Ala Ala Asn Leu Ser Ser Ser Ser Ala Gly Ser Lys Asp Thr Pro Ser 645 650 655			1969
tac cag tcc atg act agt ctc cat acg agc tct gag tcc att gac ctg Tyr Gln Ser Met Thr Ser Leu His Thr Ser Ser Glu Ser Ile Asp Leu 660 665 670			2017
ccc ctc agc cat cat ggc tcc ctg tct gga ctg acc aca ggc act cac Pro Leu Ser His His Gly Ser Leu Ser Gly Leu Thr Thr Gly Thr His 675 680 685			2065
gag gtg cag agc ctg ctc atg aga acg ggt agt gtg aga tct act ctc Glu Val Gln Ser Leu Leu Met Arg Thr Gly Ser Val Arg Ser Thr Leu 690 695 700			2113
tca gaa aga tac acc cca tca tct cgg cag gcc aac caa gaa gaa ggc Ser Glu Arg Tyr Thr Pro Ser Ser Arg Gln Ala Asn Gln Glu Glu Gly 705 710 715 720			2161
aaa gag tgg ctg cga tcg cat tcc act ggc ggg ctg cag gat act ggc Lys Glu Trp Leu Arg Ser His Ser Thr Gly Gly Leu Gln Asp Thr Gly 725 730 735			2209
aac cag tct ccc ttg gtc tcc cct tct gcc atg tca tcg tca gcc acc Asn Gln Ser Pro Leu Val Ser Pro Ser Ala Met Ser Ser Ser Ala Thr 740 745 750			2257
gga aaa tat cac ttt tcc aac ttg gtg agt ccc acc aac ctc tcc cag Gly Lys Tyr His Phe Ser Asn Leu Val Ser Pro Thr Asn Leu Ser Gln 755 760 765			2305
ttt aac ctg cct gca ccc agt atg atg cgc tcc agc agt atc ccc gcc			2353

Corrected Sequence Listing2.ST25

Phe	Asn	Leu	Pro	Ala	Pro	Ser	Met	Met	Arg	Ser	Ser	Ser	Ile	Pro	Ala		
770						775						780					
cag	gac	tcc	tcc	ttc	gac	ctc	tat	gat	gat	gcc	cag	ctt	tgc	ggt	agt		2401
Gln	Asp	Ser	Ser	Phe	Asp	Leu	Tyr	Asp	Asp	Ala	Gln	Leu	Cys	Gly	Ser		
785					790					795					800		
gca	act	tcc	ctg	gag	gaa	agg	cca	cgg	gcc	ggt	agc	cac	tcc	ggc	tca		2449
Ala	Thr	Ser	Leu	Glu	Glu	Arg	Pro	Arg	Ala	Val	Ser	His	Ser	Gly	Ser		
				805					810					815			
ttc	aga	gac	agc	atg	gag	gaa	ggt	cat	ggc	tct	tca	ctg	tca	ttg	gtc		2497
Phe	Arg	Asp	Ser	Met	Glu	Glu	Val	His	Gly	Ser	Ser	Leu	Ser	Leu	Val		
			820					825					830				
tcc	agc	aca	tca	tcc	ctt	tac	tct	acg	gct	gaa	gag	aag	gct	cat	tca		2545
Ser	Ser	Thr	Ser	Ser	Leu	Tyr	Ser	Thr	Ala	Glu	Glu	Lys	Ala	His	Ser		
		835					840					845					
gag	caa	atc	cat	aag	cta	cgg	aga	gaa	ctg	ggt	gcc	tcc	cag	gag	aaa		2593
Glu	Gln	Ile	His	Lys	Leu	Arg	Arg	Glu	Leu	Val	Ala	Ser	Gln	Glu	Lys		
	850					855					860						
gtc	gct	acc	ctc	acg	tct	cag	ctg	tca	gca	aat	gct	cac	ctt	gta	gca		2641
Val	Ala	Thr	Leu	Thr	Ser	Gln	Leu	Ser	Ala	Asn	Ala	His	Leu	Val	Ala		
	865				870					875					880		
gct	ttt	gaa	aag	agt	tta	ggg	aat	atg	act	ggc	cgt	ttg	caa	agt	cta		2689
Ala	Phe	Glu	Lys	Ser	Leu	Gly	Asn	Met	Thr	Gly	Arg	Leu	Gln	Ser	Leu		
				885					890					895			
acc	atg	aca	gcg	gaa	caa	aag	gaa	tct	gag	ctt	atc	gaa	ctg	cgg	gaa		2737
Thr	Met	Thr	Ala	Glu	Gln	Lys	Glu	Ser	Glu	Leu	Ile	Glu	Leu	Arg	Glu		
			900					905					910				
acc	att	gaa	atg	ttg	aag	gcc	cag	aac	tct	gct	gcc	caa	gca	gcc	att		2785
Thr	Ile	Glu	Met	Leu	Lys	Ala	Gln	Asn	Ser	Ala	Ala	Gln	Ala	Ala	Ile		
		915					920					925					
cag	gga	gca	ctg	aat	ggc	cca	gac	cac	cct	ccc	aaa	gat	ctc	cgc	atc		2833
Gln	Gly	Ala	Leu	Asn	Gly	Pro	Asp	His	Pro	Pro	Lys	Asp	Leu	Arg	Ile		
	930					935					940						
aga	aga	cag	cac	tcc	tct	gaa	agt	ggt	tct	agt	atc	aac	agc	gca	acg		2881
Arg	Arg	Gln	His	Ser	Ser	Glu	Ser	Val	Ser	Ser	Ile	Asn	Ser	Ala	Thr		
	945				950					955					960		
agc	cat	tcc	agc	att	ggc	agt	ggt	aat	gat	gct	gac	tcc	aag	aaa			2926
Ser	His	Ser	Ser	Ile	Gly	Ser	Gly	Asn	Asp	Ala	Asp	Ser	Lys	Lys			
				965					970					975			

<210> 20
 <211> 975
 <212> PRT
 <213> Mouse

<400> 20

Ser	His	Ser	Thr	Leu	Glu	Thr	Thr	Phe	Asp	Thr	Thr	Val	Thr	Thr	Glu	
1				5				10							15	

Corrected Sequence Listing2.ST25

Val Asn Gly Arg Ala Ile Pro Asn Leu Thr Ser Arg Pro Ser Pro Met
20 25 30

Thr Trp Arg Leu Gly Gln Ala Cys Pro Arg Leu Gln Ala Gly Asp Ala
35 40 45

Pro Ser Met Gly Ala Gly Tyr Ser Arg Ser Gly Thr Ser Arg Phe Ile
50 55 60

His Thr Asp Pro Ser Arg Phe Met Tyr Thr Thr Pro Leu Arg Arg Ala
65 70 75 80

Ala Val Ser Arg Leu Gly Asn Met Ser Gln Ile Asp Met Ser Glu Lys
85 90 95

Ala Ser Ser Asp Leu Asp Val Ser Ser Glu Val Asp Val Gly Gly Tyr
100 105 110

Met Ser Asp Gly Asp Ile Leu Gly Lys Ser Leu Arg Ala Asp Asp Ile
115 120 125

Asn Ser Gly Tyr Met Thr Asp Gly Gly Leu Asn Leu Tyr Thr Arg Ser
130 135 140

Leu Asn Arg Val Pro Asp Thr Ala Thr Ser Arg Asp Val Ile Gln Arg
145 150 155 160

Gly Val His Asp Val Thr Val Asp Ala Asp Ser Trp Asp Asp Ser Ser
165 170 175

Ser Val Ser Ser Gly Leu Ser Asp Thr Leu Asp Asn Ile Ser Thr Asp
180 185 190

Asp Leu Asn Thr Thr Ser Ser Ile Ser Ser Tyr Ser Asn Ile Thr Val
195 200 205

Pro Ser Arg Lys Asn Thr Gln Leu Lys Thr Asp Ala Glu Lys Arg Ser
210 215 220

Thr Thr Asp Glu Thr Trp Asp Ser Pro Glu Glu Leu Lys Lys Ala Glu
225 230 235 240

Gly Asp Cys Asp Ser His Gly Asp Gly Ala Ala Lys Trp Lys Gly Ala
245 250 255

Thr Ser Gly Leu Ala Glu Asp Ser Glu Lys Thr Gly Gln Lys Ala Ser
260 265 270

Corrected Sequence Listing2.ST25

Leu Ser Val Ser Gln Thr Gly Ser Trp Arg Arg Gly Met Ser Ala Gln
275 280 285

Gly Gly Thr Pro Ala Thr Ala Arg Gln Lys Thr Ser Thr Ser Ala Leu
290 295 300

Lys Thr Pro Gly Lys Thr Asp Asp Ala Lys Ala Ser Glu Lys Gly Lys
305 310 315 320

Thr Pro Leu Lys Gly Ser Ser Leu Gln Arg Ser Pro Ser Asp Ala Gly
325 330 335

Lys Ser Ser Gly Asp Glu Gly Lys Lys Pro Pro Ser Gly Ile Gly Arg
340 345 350

Ser Thr Ala Ser Ser Ser Phe Gly Tyr Lys Lys Pro Ser Gly Val Gly
355 360 365

Ala Ser Thr Met Ile Thr Ser Ser Gly Ala Thr Ile Thr Ser Gly Ser
370 375 380

Ala Thr Leu Gly Lys Ile Pro Lys Ser Ala Ala Ile Gly Gly Lys Ser
385 390 395 400

Asn Ala Gly Arg Lys Thr Ser Leu Asp Gly Ser Gln Asn Gln Asp Asp
405 410 415

Val Val Leu His Val Ser Ser Lys Thr Thr Leu Gln Tyr Arg Ser Leu
420 425 430

Pro Arg Pro Ser Lys Ser Ser Thr Ser Gly Ile Pro Gly Arg Gly Gly
435 440 445

His Arg Ser Ser Thr Ser Ser Ile Asp Ser Asn Val Ser Ser Lys Ser
450 455 460

Ala Gly Ala Thr Thr Ser Lys Leu Arg Glu Pro Thr Lys Ile Gly Ser
465 470 475 480

Gly Arg Ser Ser Pro Val Thr Val Asn Gln Thr Asp Lys Glu Lys Glu
485 490 495

Lys Val Ala Val Ser Asp Ser Glu Ser Val Ser Leu Ser Gly Ser Pro
500 505 510

Lys Ser Ser Pro Thr Ser Ala Ser Ala Cys Gly Thr Gln Gly Leu Arg
515 520 525

Corrected Sequence Listing2.ST25

Gln Pro Gly Ser Lys Tyr Pro Asp Ile Ala Ser Pro Thr Phe Arg Arg
530 535 540

Leu Phe Gly Ala Lys Ala Gly Gly Lys Ser Ala Ser Ala Pro Asn Thr
545 550 555 560

Glu Gly Ala Lys Ser Ser Ser Val Val Leu Ser Pro Ser Thr Ser Leu
565 570 575

Ala Arg Gln Gly Ser Leu Glu Ser Pro Ser Ser Gly Thr Gly Ser Met
580 585 590

Gly Ser Ala Gly Gly Leu Ser Gly Ser Ser Ser Pro Leu Phe Asn Lys
595 600 605

Pro Ser Asp Leu Thr Thr Asp Val Ile Ser Leu Ser His Ser Leu Ala
610 615 620

Ser Ser Pro Ala Ser Val His Ser Phe Thr Ser Gly Gly Leu Val Trp
625 630 635 640

Ala Ala Asn Leu Ser Ser Ser Ser Ala Gly Ser Lys Asp Thr Pro Ser
645 650 655

Tyr Gln Ser Met Thr Ser Leu His Thr Ser Ser Glu Ser Ile Asp Leu
660 665 670

Pro Leu Ser His His Gly Ser Leu Ser Gly Leu Thr Thr Gly Thr His
675 680 685

Glu Val Gln Ser Leu Leu Met Arg Thr Gly Ser Val Arg Ser Thr Leu
690 695 700

Ser Glu Arg Tyr Thr Pro Ser Ser Arg Gln Ala Asn Gln Glu Glu Gly
705 710 715 720

Lys Glu Trp Leu Arg Ser His Ser Thr Gly Gly Leu Gln Asp Thr Gly
725 730 735

Asn Gln Ser Pro Leu Val Ser Pro Ser Ala Met Ser Ser Ser Ala Thr
740 745 750

Gly Lys Tyr His Phe Ser Asn Leu Val Ser Pro Thr Asn Leu Ser Gln
755 760 765

Phe Asn Leu Pro Ala Pro Ser Met Met Arg Ser Ser Ser Ile Pro Ala

Corrected Sequence Listing2.ST25
775 780

770

Gln Asp Ser Ser Phe Asp Leu Tyr Asp Asp Ala Gln Leu Cys Gly Ser
785 790 795 800

Ala Thr Ser Leu Glu Glu Arg Pro Arg Ala Val Ser His Ser Gly Ser
805 810 815

Phe Arg Asp Ser Met Glu Glu Val His Gly Ser Ser Leu Ser Leu Val
820 825 830

Ser Ser Thr Ser Ser Leu Tyr Ser Thr Ala Glu Glu Lys Ala His Ser
835 840 845

Glu Gln Ile His Lys Leu Arg Arg Glu Leu Val Ala Ser Gln Glu Lys
850 855 860

Val Ala Thr Leu Thr Ser Gln Leu Ser Ala Asn Ala His Leu Val Ala
865 870 875 880

Ala Phe Glu Lys Ser Leu Gly Asn Met Thr Gly Arg Leu Gln Ser Leu
885 890 895

Thr Met Thr Ala Glu Gln Lys Glu Ser Glu Leu Ile Glu Leu Arg Glu
900 905 910

Thr Ile Glu Met Leu Lys Ala Gln Asn Ser Ala Ala Gln Ala Ala Ile
915 920 925

Gln Gly Ala Leu Asn Gly Pro Asp His Pro Pro Lys Asp Leu Arg Ile
930 935 940

Arg Arg Gln His Ser Ser Glu Ser Val Ser Ser Ile Asn Ser Ala Thr
945 950 955 960

Ser His Ser Ser Ile Gly Ser Gly Asn Asp Ala Asp Ser Lys Lys
965 970 975

<210> 21
<211> 2583
<212> DNA
<213> Mouse

<400> 21
gggatgaagg gaaaaagcca ccgtcaggca ttggaagatc gacagccagc agttcttttg 60
gatacaagaa gccaaagtgt gtaggggctt ccactatgat taccagcagc ggtgccacca 120
tcacaagcgg ttcagctaca ctgggggaaaa tccccaaatc cgctgccatt ggtgggaagt 180

Corrected Sequence Listing2.ST25

ccaatgcagg aaggaaaacc agcctggacg ggtcccagaa tcaagatgat gttgtcctgc	240
acgtgagctc gaagaccacc ctccagtacc gtagtttgcc ccgccccttct aagtccagca	300
ccagcggaaat ccctgggaga ggtggccaca ggtcgagcac cagcagcatt gattccaatg	360
tcagcagcaa gtcagctggg gccaccacct ccaaactgag agaaccgact aagatcggct	420
cagggcgctc gagtccagtc actgtcaacc aaacagacaa agagaaggag aaagtagcag	480
tgtcagattc agagagcggt tccttgtcag gttcccccaa atccagcccc acctctgcc	540
gtgcctgtgg gactcaaggg ctccagacagc caggggtccaa atatccagat attgcctcgc	600
ccacatttcg aaggtaaggg tatgtaaaga gatgttggga aaacataaaa ggtagtatat	660
agcatgtatt tattctgtac gaaactatct tcatgtattc taaatattct aagattctgt	720
atcttatact tgtctaaaat atagtgtatt tattttgctg attgcacctg ttgctagtgt	780
aaaagcattg ctcatcttaga gagtgggttag cctttcagct atacagccag tgtgacacta	840
aaatacagat accacttgta gcgggcataa aaccacatga ctgactattc atagaaataa	900
agtgatagct tgtaaagata tttagtgtatt tccacctctc ctttccagaa ttaaaaaaag	960
caaattgcat agatctttat aaacacattt acttctagtgt tatgtttatct tgttgactct	1020
taatgaaatg gcagttatga atatagatga tatattcttt ctaacagttt ataagagacc	1080
aattttatata gtaccagatc ttaacatagt aacaataaca gcaacaaaaa caacccaaaa	1140
agctatcaaa gtatgggtctg attgcagaat ttgaaaacat ttacatgttt gacataggac	1200
aagaactcag gagtgaggtg actttttata agtcttcac aatgtccttt tacaggaacc	1260
aggaagcata tctgatatat gtgtcaggat tatcacttta ttaattatgt gaaattctgt	1320
ttagaaatct acctgatttt aaatacttta atatagtagg ggtcaaaatt agttaatgag	1380
ttaagacaag ttgttaaata atcctggctc tgttttctca tcttcaaaat gatagagtat	1440
aattttatcac ctcttggtta atatttcagg tttgtgttta ttctcttgat aactttgatc	1500
tcttagaaga gtcttgaaga atttacatta agtaatctta gaaacataac tatttgagaa	1560
acagtagtca aattttgtca ttagaagtat taactctgaa gaatgatttg aagtgcagct	1620
tcttagaaaag aataaattat agcttgtagc aagagtaaatt attttctctg cttgtgtgag	1680
agccaagagc gccctcttgt ggccattac ctatgaaaca atttctcata ttcgccctag	1740
aaatcttcca ctgcaggaaa taatggattt cattgcctct gaattagtaa ccattctgcc	1800
atcttctcat accattttat ttccatactt gcataaattt gattatgtca tctgcttcat	1860
ttacaaaact aaaatgtttt ctgagctaaa ctccagtagc taacttagta caaatggtat	1920
ttttaaatca ctgctataag tatatatatt tgaatagctc tggcaacgga cggaaatccc	1980
tatgggtctt ccatgggaag atacaaacca atccataagt tgtccagcaa tatccaatat	2040
ttccagccca gccagtcagg cctcttaaac attaccttac atatttgaac ctttccttaa	2100

Corrected Sequence Listing2.ST25

```

atgtccccctt tagacaatct attttttaaa aagatgaaaa tccatttaag catcatatat 2160
cgaatgcgta gaagttgttt cattataatg gttctgcaga taggtaatgc caaaacggcc 2220
aaaatatttg atcactagaa gcgtaaaagt caagtacaat catgttgact ttttttccaa 2280
ggtgggttca ctgctgcccc ccttggttcc aggccagtgc ttacttaaga tatcgtaagt 2340
gatttttttt taatttttaa ttttttagta gttggttaat caaaagccag tcatgtcacc 2400
ttcaggaaca tagaggctgg acgtgcttgg cagctcacga ctcaaagca cacttggtc 2460
tgtggactga aaccctagga aacgtggatg tgagtctctt ggaacaactc aagttgttat 2520
ttgtttttct tttaggttgt tcggtgccaa ggcaggcggc aaatctgcct ccgcacctaa 2580
tac 2583

```

```

<210> 22
<211> 37
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> (2)..(34)
<223>

```

```

<400> 22
c cgc ggg gct tcc atc ctt cct ttg act gat ttt taa 37
  Arg Gly Ala Ser Ile Leu Pro Leu Thr Asp Phe
    1             5             10

```

```

<210> 23
<211> 6768
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> (1)..(5928)
<223>

```

```

<400> 23
att tta att tgt att ttc ccc gcc gcc ccg ccc ctt ttc ctc cga ccc 48
Ile Leu Ile Cys Ile Phe Pro Ala Ala Pro Pro Leu Phe Leu Arg Pro
 1             5             10             15

```

```

cgc cct atc gct ccc cgg ctt ccc tgc tct ttc ctt ttt ccc ggc ttc 96
Arg Pro Ile Ala Pro Arg Leu Pro Cys Ser Phe Leu Phe Pro Gly Phe
          20             25             30

```

```

ctt cct cgc gtt tct ttc ccc tgc gcc ctc ggc ttg cct ctc tcc ctc 144
Leu Pro Arg Val Ser Phe Pro Cys Ala Leu Gly Leu Pro Leu Ser Leu
          35             40             45

```

```

ctc cct cgc tct ctc ccc ctt ctc tcc cct tct tcc tcg gtt tct tcc 192
Leu Pro Arg Ser Leu Pro Leu Leu Ser Pro Ser Ser Ser Val Ser Ser
    50             55             60

```

Corrected Sequence Listing2.ST25

gtc ctc tct ctc ccc ctc ctc ctc cgc ctc ctc ctc ctg cgc tcc Val Leu Ser Leu Pro Leu Leu Pro Arg Leu Leu Leu Arg Ser 65 70 75 80	240
cgc ccc ctg ccc cct ccc ccc gtg cct gca gac gcg cgg atc gtc cat Arg Pro Leu Pro Pro Pro Pro Val Pro Ala Asp Ala Arg Ile Val His 85 90 95	288
gcg ctc ctc gcg ggc aga atg ctg ggc agc agc gtc aag agc gtg cag Ala Leu Leu Ala Gly Arg Met Leu Gly Ser Ser Val Lys Ser Val Gln 100 105 110	336
ccc gag gtg gag ctg agc agc ggc ggc ggc gac gag ggc gcg gac gaa Pro Glu Val Glu Leu Ser Ser Gly Gly Gly Asp Glu Gly Ala Asp Glu 115 120 125	384
ccg cgg ggc gcc ggc agg aag gcg gca gcg gcg gac ggc aga ggc atg Pro Arg Gly Ala Gly Arg Lys Ala Ala Ala Asp Gly Arg Gly Met 130 135 140	432
ctg ccc aag cgc gcc aag gcg ccc ggc ggc ggc ggc ggc atg gcc aag Leu Pro Lys Arg Ala Lys Ala Pro Gly Gly Gly Gly Gly Met Ala Lys 145 150 155 160	480
gcc agc gcg gct gag ctg aag gtc ttc aag tcc ggc agc gtg gac agc Ala Ser Ala Ala Glu Leu Lys Val Phe Lys Ser Gly Ser Val Asp Ser 165 170 175	528
cgt gtc ccc ggc ggc ccg ccc gcc tcc aac ctg cgc aag cag aag tca Arg Val Pro Gly Gly Pro Pro Ala Ser Asn Leu Arg Lys Gln Lys Ser 180 185 190	576
ctc acc aac ctc tct ttt ctc acg gac tcc gag aaa aag ctg cag ctt Leu Thr Asn Leu Ser Phe Leu Thr Asp Ser Glu Lys Lys Leu Gln Leu 195 200 205	624
tat gag ccc gaa tgg agc gac gat atg gcc aag gcg ccc aaa ggc tta Tyr Glu Pro Glu Trp Ser Asp Asp Met Ala Lys Ala Pro Lys Gly Leu 210 215 220	672
ggc aag gtg ggc tcc aag ggc cgt gaa gct ccg ctg atg tcc aag acg Gly Lys Val Gly Ser Lys Gly Arg Glu Ala Pro Leu Met Ser Lys Thr 225 230 235 240	720
ctg tcc aag tcg gag cac tcg ctc ttc cag gcc aag ggc agc ccg gcg Leu Ser Lys Ser Glu His Ser Leu Phe Gln Ala Lys Gly Ser Pro Ala 245 250 255	768
ggc ggc gcc aag acc ccc ctg gct ccg ctc gcg ccc aac ctg gga aag Gly Gly Ala Lys Thr Pro Leu Ala Pro Leu Ala Pro Asn Leu Gly Lys 260 265 270	816
ccg agc cgg atc cct cga gga ccc tat gcg gag gtc aag ccg ctc agc Pro Ser Arg Ile Pro Arg Gly Pro Tyr Ala Glu Val Lys Pro Leu Ser 275 280 285	864
aag gcg cct gaa gcg gcc gtg agc gaa gat ggc aaa tcg gac gac gag Lys Ala Pro Glu Ala Ala Val Ser Glu Asp Gly Lys Ser Asp Asp Glu 290 295 300	912
ctg ctc tcc agc aag gcc aag gcg caa aag agc tct ggg cct gtc ccc Leu Leu Ser Ser Lys Ala Lys Ala Gln Lys Ser Ser Gly Pro Val Pro 305 310 315 320	960

Corrected Sequence Listing2.ST25

tct gcc aag ggc cag gag gag cgc gcc ttc ctc aag gtg gac ccc gag Ser Ala Lys Gly Gln Glu Glu Arg Ala Phe Leu Lys Val Asp Pro Glu 325 330 335	1008
ctg gtg gtg acc gtg ctg gga gac ctg gag cag ctg ctc ttc agc cag Leu Val Val Thr Val Leu Gly Asp Leu Glu Gln Leu Leu Phe Ser Gln 340 345 350	1056
atg ctg gac cca gag tcc cag aga aag agg aca gtg cag aat gtc ctg Met Leu Asp Pro Glu Ser Gln Arg Lys Arg Thr Val Gln Asn Val Leu 355 360 365	1104
gat ctc cgg cag aac ctg gaa gag acc atg tcc agc ctg cga ggg tcc Asp Leu Arg Gln Asn Leu Glu Glu Thr Met Ser Ser Leu Arg Gly Ser 370 375 380	1152
cag gtg act cac agc tcc ctg gag atg acc tgc tac gac agc gat gat Gln Val Thr His Ser Ser Leu Glu Met Thr Cys Tyr Asp Ser Asp Asp 385 390 400	1200
gcc aac cca cgc agc gtg tcc agc ctc tcc aac cgc tcg tac cct ctg Ala Asn Pro Arg Ser Val Ser Ser Leu Ser Asn Arg Ser Tyr Pro Leu 405 410 415	1248
tca tgg cgc tat ggc cag tcc agt ccg cgg ctg cag gct ggt gac gcg Ser Trp Arg Tyr Gly Gln Ser Ser Pro Arg Leu Gln Ala Gly Asp Ala 420 425 430	1296
ccc tct gtg ggt ggg agc tgc cgc tcg gag ggg acg ccc gcc tgg tac Pro Ser Val Gly Gly Ser Cys Arg Ser Glu Gly Thr Pro Ala Trp Tyr 435 440 445	1344
atg cac ggc gaa cgg gcc cac tac tcc cac acc atg ccc atg cgc agc Met His Gly Glu Arg Ala His Tyr Ser His Thr Met Pro Met Arg Ser 450 455 460	1392
ccc agc aag ctc agc cat atc tcc cgc ctg gag ctg gtc gaa tcc ctg Pro Ser Lys Leu Ser His Ile Ser Arg Leu Glu Leu Val Glu Ser Leu 465 470 475 480	1440
gac tcg gat gag gtg gac ctc aag tcc ggc tac atg agc gac agt gac Asp Ser Asp Glu Val Asp Leu Lys Ser Gly Tyr Met Ser Asp Ser Asp 485 490 495	1488
ctc atg ggc aag acc atg acg gag gat gat gac atc act acc ggc tgg Leu Met Gly Lys Thr Met Thr Glu Asp Asp Asp Ile Thr Thr Gly Trp 500 505 510	1536
gat gaa agc agc tcc atc agt agt gga ctc agc gat gcc tca gac aat Asp Glu Ser Ser Ser Ile Ser Ser Gly Leu Ser Asp Ala Ser Asp Asn 515 520 525	1584
ctc agt tca gaa gaa ttc aat gcc agc tcc tca ctc aac tcc ctc cca Leu Ser Ser Glu Glu Phe Asn Ala Ser Ser Ser Leu Asn Ser Leu Pro 530 535 540	1632
agt act ccc act gct tct cgc agg aac tca aca ata gtg cta cgc aca Ser Thr Pro Thr Ala Ser Arg Arg Asn Ser Thr Ile Val Leu Arg Thr 545 550 555 560	1680
gac tca gag aag cgc tca ctg gca gaa agt ggg ctg agc tgg ttt agt Asp Ser Glu Lys Arg Ser Leu Ala Glu Ser Gly Leu Ser Trp Phe Ser 565 570 575 580	1728

Corrected Sequence Listing2.ST25

565	570	575	
gaa tca gag gag aaa gcc cct aaa aaa ctg gag tac gac agt ggt agc Glu Ser Glu Glu Lys Ala Pro Lys Lys Leu Glu Tyr Asp Ser Gly Ser 580 585 590			1776
ctg aag atg gaa cct ggg act tct aag tgg cgg agg gag cgg cct gag Leu Lys Met Glu Pro Gly Thr Ser Lys Trp Arg Arg Glu Arg Pro Glu 595 600 605			1824
agc tgt gat gat tca tcc aag ggt gga gaa ctg aaa aag ccc atc agc Ser Cys Asp Asp Ser Ser Lys Gly Gly Glu Leu Lys Lys Pro Ile Ser 610 615 620			1872
ctg ggc cac cct ggt tcc ctg aag aag ggc aag acc cca cct gtg gct Leu Gly His Pro Gly Ser Leu Lys Lys Gly Lys Thr Pro Pro Val Ala 625 630 635 640			1920
gta act tcc ccc atc act cac aca gcc cag agt gcc ctc aaa gtc gca Val Thr Ser Pro Ile Thr His Thr Ala Gln Ser Ala Leu Lys Val Ala 645 650 655			1968
ggc aaa cct gag ggc aaa gct aca gac aag ggt aag ctt gca gtg aag Gly Lys Pro Glu Gly Lys Ala Thr Asp Lys Gly Lys Leu Ala Val Lys 660 665 670			2016
aat act ggg ctc caa cgc tcc tcc tct gat gct ggt cgg gac cgc ctg Asn Thr Gly Leu Gln Arg Ser Ser Ser Asp Ala Gly Arg Asp Arg Leu 675 680 685			2064
agt gat gct aag aag ccc ccc tct ggc att gct cgc ccc tcc act tcg Ser Asp Ala Lys Lys Pro Pro Ser Gly Ile Ala Arg Pro Ser Thr Ser 690 695 700			2112
gga tcc ttt ggc tac aag aag cct cct cct gcc aca ggc aca gcc act Gly Ser Phe Gly Tyr Lys Lys Pro Pro Pro Ala Thr Gly Thr Ala Thr 705 710 715 720			2160
gtc atg caa act ggt ggt tca gcc act ctc agc aag atc cag aag tcc Val Met Gln Thr Gly Gly Ser Ala Thr Leu Ser Lys Ile Gln Lys Ser 725 730 735			2208
tca ggc atc cct gtc aag cca gta aat ggg cgc aag act agc tta gat Ser Gly Ile Pro Val Lys Pro Val Asn Gly Arg Lys Thr Ser Leu Asp 740 745 750			2256
gtt tcc aac agt gca gag cca gga ttc ctg gct cct gga gcc cgt tct Val Ser Asn Ser Ala Glu Pro Gly Phe Leu Ala Pro Gly Ala Arg Ser 755 760 765			2304
aac atc cag tac cgc agc ctg ccc cgg cca gcc aag tca agt tct atg Asn Ile Gln Tyr Arg Ser Leu Pro Arg Pro Ala Lys Ser Ser Ser Met 770 775 780			2352
agc gtg acc ggc ggg cgg ggt gga cct cgc cct gtg agc agc agc att Ser Val Thr Gly Gly Arg Gly Gly Pro Arg Pro Val Ser Ser Ser Ile 785 790 800			2400
gac ccc agt ctc ctc agc acc aag cag gga ggc ctt acg cct tcc aga Asp Pro Ser Leu Leu Ser Thr Lys Gln Gly Gly Leu Thr Pro Ser Arg 805 810 815			2448
ctg aag gag cct acc aag gta gcc agt ggg cgg acc act cca gcc cct			2496

Corrected Sequence Listing2.ST25

Leu	Lys	Glu	Pro	Thr	Lys	Val	Ala	Ser	Gly	Arg	Thr	Thr	Pro	Ala	Pro		
			820					825					830				
gtc	aat	cag	aca	gat	cgg	gaa	aag	gag	aag	gcc	aaa	gcc	aag	gca	gtg	2544	
Val	Asn	Gln	Thr	Asp	Arg	Glu	Lys	Glu	Lys	Ala	Lys	Ala	Lys	Ala	Val		
		835					840					845					
gcc	ttg	gac	tca	gac	aac	atc	tcc	ttg	aag	agt	att	ggc	tcc	cca	gaa	2592	
Ala	Leu	Asp	Ser	Asp	Asn	Ile	Ser	Leu	Lys	Ser	Ile	Gly	Ser	Pro	Glu		
	850					855					860						
agt	act	ccc	aag	aac	caa	gca	agc	cac	ccc	aca	gcc	acc	aag	ctg	gca	2640	
Ser	Thr	Pro	Lys	Asn	Gln	Ala	Ser	His	Pro	Thr	Ala	Thr	Lys	Leu	Ala		
865					870				875						880		
gag	ctg	cca	cca	acc	cct	ctc	agg	gcc	aca	gcg	aag	agc	ttt	gtc	aaa	2688	
Glu	Leu	Pro	Pro	Thr	Pro	Leu	Arg	Ala	Thr	Ala	Lys	Ser	Phe	Val	Lys		
				885				890						895			
cca	ccc	tca	cta	gcc	aat	ctt	gac	aag	gtc	aac	tcc	aac	agt	ctg	gat	2736	
Pro	Pro	Ser	Leu	Ala	Asn	Leu	Asp	Lys	Val	Asn	Ser	Asn	Ser	Leu	Asp		
			900					905					910				
cta	cca	tca	tcc	agt	gat	acc	acc	cat	gct	tca	aag	gtc	cca	gat	ctg	2784	
Leu	Pro	Ser	Ser	Ser	Asp	Thr	Thr	His	Ala	Ser	Lys	Val	Pro	Asp	Leu		
		915				920						925					
cat	gct	aca	agc	tca	gca	tct	ggg	ggc	cct	ctc	cct	tcc	tgc	ttc	acc	2832	
His	Ala	Thr	Ser	Ser	Ala	Ser	Gly	Gly	Pro	Leu	Pro	Ser	Cys	Phe	Thr		
	930					935					940						
ccc	agt	ccg	gca	ccc	atc	ctc	aat	att	aac	tca	gcc	agc	ttc	tcc	cag	2880	
Pro	Ser	Pro	Ala	Pro	Ile	Leu	Asn	Ile	Asn	Ser	Ala	Ser	Phe	Ser	Gln		
945					950				955						960		
ggc	ctg	gag	cta	atg	agt	ggt	ttc	agt	gtg	cca	aaa	gag	acc	cgc	atg	2928	
Gly	Leu	Glu	Leu	Met	Ser	Gly	Phe	Ser	Val	Pro	Lys	Glu	Thr	Arg	Met		
				965					970					975			
tac	ccc	aaa	ctc	tca	ggc	ctg	cac	agg	agc	atg	gag	tcc	ctc	cag	atg	2976	
Tyr	Pro	Lys	Leu	Ser	Gly	Leu	His	Arg	Ser	Met	Glu	Ser	Leu	Gln	Met		
			980					985					990				
cca	atg	agc	ctc	ccc	agt	gcc	ttc	ccc	agc	agt	act	ccc	gtc	ccc	acc	3024	
Pro	Met	Ser	Leu	Pro	Ser	Ala	Phe	Pro	Ser	Ser	Thr	Pro	Val	Pro	Thr		
		995				1000						1005					
cca	cct	gct	ccc	cct	gct	gct	ccc	aca	gaa	gaa	gag	acg	gaa	gag		3069	
Pro	Pro	Ala	Pro	Pro	Ala	Ala	Pro	Thr	Glu	Glu	Glu	Thr	Glu	Glu			
	1010					1015					1020						
ctg	act	tgg	agt	gga	agc	ccc	aga	gct	ggg	caa	ctg	gac	agt	aat		3114	
Leu	Thr	Trp	Ser	Gly	Ser	Pro	Arg	Ala	Gly	Gln	Leu	Asp	Ser	Asn			
	1025					1030					1035						
cag	cgg	gat	cgg	aac	act	ctt	ccc	aag	aaa	ggg	ctc	agg	tac	cag		3159	
Gln	Arg	Asp	Arg	Asn	Thr	Leu	Pro	Lys	Lys	Gly	Leu	Arg	Tyr	Gln			
	1040					1045					1050						
ctt	cag	tcc	cag	gag	gag	acc	aag	gag	agg	cga	cat	tcc	cat	acc		3204	
Leu	Gln	Ser	Gln	Glu	Glu	Thr	Lys	Glu	Arg	Arg	His	Ser	His	Thr			
	1055					1060					1065						

Corrected Sequence Listing2.ST25															
att Ile	ggt Gly	ggg Gly	ctg Leu	cct Pro	gaa Glu	tcc Ser	gat Asp	gac Asp	cag Gln	tca Ser	gag Glu	ctg Leu	cct Pro	tct Ser	3249
1070						1075					1080				
ccc Pro	cct Pro	gca Ala	ctt Leu	ccc Pro	atg Met	tct Ser	ctg Leu	agt Ser	gca Ala	aag Lys	ggc Gly	caa Gln	ctt Leu	acc Thr	3294
1085						1090					1095				
aac Asn	ata Ile	gtg Val	agt Ser	ccc Pro	act Thr	gcg Ala	gcc Ala	acc Thr	acg Thr	cca Pro	aga Arg	atc Ile	acc Thr	cgc Arg	3339
1100						1105					1110				
tcc Ser	aac Asn	agc Ser	atc Ile	ccc Pro	acc Thr	cac His	gag Glu	gcg Ala	gcc Ala	ttc Phe	gag Glu	ctg Leu	tac Tyr	agc Ser	3384
1115						1120					1125				
ggc Gly	tcc Ser	caa Gln	atg Met	ggg Gly	agc Ser	acc Thr	ctg Leu	tcc Ser	ctg Leu	gcc Ala	gag Glu	aga Arg	ccc Pro	aag Lys	3429
1130						1135					1140				
gga Gly	atg Met	att Ile	cgg Arg	tca Ser	gga Gly	tcc Ser	ttc Phe	cga Arg	gac Asp	ccc Pro	acg Thr	gac Asp	gat Asp	gtt Val	3474
1145						1150					1155				
cac His	ggc Gly	tca Ser	gtg Val	ctg Leu	tcc Ser	ctg Leu	gcc Ala	tcc Ser	agt Ser	gcc Ala	tcc Ser	tcc Ser	acc Thr	tac Tyr	3519
1160						1165					1170				
tcc Ser	tca Ser	gct Ala	gag Glu	gag Glu	agg Arg	atg Met	caa Gln	tct Ser	gag Glu	caa Gln	atc Ile	cgg Arg	aag Lys	ctt Leu	3564
1175						1180					1185				
cgt Arg	agg Arg	gaa Glu	ctg Leu	gaa Glu	tca Ser	tcc Ser	cag Gln	gaa Glu	aaa Lys	gtg Val	gcc Ala	acc Thr	ttg Leu	acg Thr	3609
1190						1195					1200				
tct Ser	cag Gln	ctt Leu	tct Ser	gcc Ala	aat Asn	gct Ala	aat Asn	ctg Leu	gtg Val	gct Ala	gct Ala	ttt Phe	gag Glu	cag Gln	3654
1205						1210					1215				
agc Ser	ctg Leu	gtg Val	aat Asn	atg Met	aca Thr	tcc Ser	cgc Arg	ctg Leu	cga Arg	cac His	ctg Leu	gca Ala	gag Glu	acg Thr	3699
1220						1225					1230				
gcc Ala	gag Glu	gag Glu	aag Lys	gac Asp	act Thr	gag Glu	ctg Leu	ctg Leu	gat Asp	ttg Leu	cga Arg	gaa Glu	acc Thr	ata Ile	3744
1235						1240					1245				
gac Asp	ttt Phe	ctg Leu	aag Lys	aaa Lys	aag Lys	aac Asn	tct Ser	gag Glu	gcc Ala	cag Gln	gca Ala	gtc Val	att Ile	cag Gln	3789
1250						1255					1260				
gga Gly	gcc Ala	ctt Leu	aat Asn	gcc Ala	tca Ser	gaa Glu	acc Thr	aca Thr	ccc Pro	aaa Lys	gaa Glu	ctt Leu	cgg Arg	atc Ile	3834
1265						1270					1275				
aag Lys	aga Arg	caa Gln	aac Asn	tcc Ser	tca Ser	gat Asp	agc Ser	atc Ile	tca Ser	agc Ser	ctc Leu	aac Asn	agc Ser	atc Ile	3879
1280						1285					1290				
act Thr	agc Ser	cat His	tcc Ser	agc Ser	atc Ile	ggc Gly	agc Ser	agc Ser	aag Lys	gat Asp	gct Ala	gat Asp	gcg Ala	aaa Lys	3924
1295						1300					1305				

Corrected Sequence Listing2.ST25

aag Lys	aag Lys 1310	aaa Lys	aaa Lys	aag Lys	agt Ser	tgg Trp 1315	ctt Leu	cga Arg	agt Ser	tcc Ser	ttc Phe 1320	aac Asn	aaa Lys	gcg Ala	3969
ttc Phe	agt Ser 1325	ata Ile	aaa Lys	aag Lys	ggg Gly	ccc Pro 1330	aag Lys	tca Ser	gct Ala	tcc Ser	tca Ser 1335	tac Tyr	tcg Ser	gat Asp	4014
ata Ile	gag Glu 1340	gag Glu	att Ile	gct Ala	aca Thr	ccc Pro 1345	gac Asp	tct Ser	tca Ser	gcc Ala	ccc Pro 1350	tca Ser	tcc Ser	ccc Pro	4059
aaa Lys	cta Leu 1355	cag Gln	cat His	ggt Gly	tct Ser	aca Thr 1360	gag Glu	act Thr	gct Ala	tca Ser	ccc Pro 1365	tcc Ser	atc Ile	aag Lys	4104
tcc Ser	tcc Ser 1370	acc Thr	tcg Ser	tcc Ser	tcc Ser	gtg Val 1375	ggc Gly	act Thr	gat Asp	gtc Val	acc Thr 1380	gag Glu	ggc Gly	cct Pro	4149
gct Ala	cac His 1385	cca Pro	gcc Ala	ccc Pro	cac His	act Thr 1390	agg Arg	ctg Leu	ttc Phe	cat His	gca Ala 1395	aat Asn	gag Glu	gag Glu	4194
gag Glu	gag Glu 1400	cca Pro	gag Glu	aag Lys	aag Lys	gag Glu 1405	gta Val	tcg Ser	gag Glu	ctg Leu	cgc Arg 1410	tct Ser	gag Glu	cta Leu	4239
tgg Trp	gag Glu 1415	aag Lys	gaa Glu	atg Met	aag Lys	ctt Leu 1420	aca Thr	gac Asp	atc Ile	cgc Arg	ttg Leu 1425	gag Glu	gcc Ala	ctc Leu	4284
aac Asn	tct Ser 1430	gcc Ala	cac His	caa Gln	ctg Leu	gat Asp 1435	cag Gln	ctt Leu	cgg Arg	gag Glu	acc Thr 1440	atg Met	cac His	aac Asn	4329
atg Met	cag Gln 1445	ttg Leu	gag Glu	gtg Val	gac Asp	ctg Leu 1450	ctg Leu	gaa Glu	gca Ala	gag Glu	aat Asn 1455	gac Asp	cga Arg	ctg Leu	4374
aag Lys	gta Val 1460	gcc Ala	cca Pro	ggc Gly	ccc Pro	tca Ser 1465	tca Ser	ggc Gly	tcc Ser	act Thr	cca Pro 1470	ggg Gly	cag Gln	gtc Val	4419
cct Pro	gga Gly 1475	tca Ser	tct Ser	gca Ala	tta Leu	tct Ser 1480	tcc Ser	cca Pro	cgc Arg	cgc Arg	tcc Ser 1485	cta Leu	ggc Gly	ctg Leu	4464
gca Ala	ctc Leu 1490	acc Thr	cat His	tcc Ser	ttc Phe	ggc Gly 1495	ccc Pro	agt Ser	ctt Leu	gca Ala	gac Asp 1500	aca Thr	gac Asp	ctg Leu	4509
tca Ser	ccc Pro 1505	atg Met	gat Asp	ggc Gly	atc Ile	agt Ser 1510	act Thr	tgt Cys	ggc Gly	cca Pro	aag Lys 1515	gag Glu	gaa Glu	gtg Val	4554
acc Thr	ctc Leu 1520	cgg Arg	gtg Val	gtg Val	gtg Val	agg Arg 1525	atg Met	ccc Pro	ccg Pro	cag Gln	cac His 1530	atc Ile	atc Ile	aaa Lys	4599
ggg Gly	gac Asp	ttg Leu	aag Lys	cag Gln	cag Gln	gaa Glu	ttc Phe	ttc Phe	ctg Leu	ggc Gly	tgt Cys	agc Ser	aag Lys	gtc Val	4644

Corrected Sequence Listing2.ST25															
1535	1540										1545				
agt gga aaa gtt gac tgg aag atg ctg gat gaa gct gtt ttc caa	4689														
Ser Gly Lys Val Asp Trp Lys Met Leu Asp Glu Ala Val Phe Gln															
1550	1555	1560													
gtg ttc aag gac tat att tct aaa atg gac cca gcc tct acc ctg	4734														
Val Phe Lys Asp Tyr Ile Ser Lys Met Asp Pro Ala Ser Thr Leu															
1565	1570	1575													
gga cta agc act gag tcc atc cat ggc tac agc atc agc cac gtg	4779														
Gly Leu Ser Thr Glu Ser Ile His Gly Tyr Ser Ile Ser His Val															
1580	1585	1590													
aaa cga gtg ttg gat gca gag ccc ccc gag atg cct cct tgc cgt	4824														
Lys Arg Val Leu Asp Ala Glu Pro Pro Glu Met Pro Pro Cys Arg															
1595	1600	1605													
cga ggt gtc aat aac ata tca gtc tcc ctc aaa ggt ctg aag gag	4869														
Arg Gly Val Asn Asn Ile Ser Val Ser Leu Lys Gly Leu Lys Glu															
1610	1615	1620													
aaa tgc gtc gac agc ctg gtg ttc gag acg ctg atc ccc aag ccg	4914														
Lys Cys Val Asp Ser Leu Val Phe Glu Thr Leu Ile Pro Lys Pro															
1625	1630	1635													
atg atg cag cac tac ata agc ctc ctg ctg aag cac cgg cgc ctc	4959														
Met Met Gln His Tyr Ile Ser Leu Leu Leu Lys His Arg Arg Leu															
1640	1645	1650													
gtc ctc tcg ggc ccc agc ggc acg ggc aag acc tac ctg acc aat	5004														
Val Leu Ser Gly Pro Ser Gly Thr Gly Lys Thr Tyr Leu Thr Asn															
1655	1660	1665													
cgc ttg gcc gag tac ctg gtg gag cgc tct ggc cgt gag gtc aca	5049														
Arg Leu Ala Glu Tyr Leu Val Glu Arg Ser Gly Arg Glu Val Thr															
1670	1675	1680													
gag ggc atc gtc agc acc ttc aac atg cac cag cag tct tgc aag	5094														
Glu Gly Ile Val Ser Thr Phe Asn Met His Gln Gln Ser Cys Lys															
1685	1690	1695													
gat ctg caa ctg tat ctt tcc aac cta gcc aac cag ata gac cgg	5139														
Asp Leu Gln Leu Tyr Leu Ser Asn Leu Ala Asn Gln Ile Asp Arg															
1700	1705	1710													
gaa aca gga att ggg gat gtg ccc ctg gtg att cta ttg gat gac	5184														
Glu Thr Gly Ile Gly Asp Val Pro Leu Val Ile Leu Leu Asp Asp															
1715	1720	1725													
ctg agt gaa gca ggc tcc atc agt gag ttg gtc aat ggg gcc ctc	5229														
Leu Ser Glu Ala Gly Ser Ile Ser Glu Leu Val Asn Gly Ala Leu															
1730	1735	1740													
acc tgc aag tat cat aaa tgt ccc tat att ata ggt acc acc aat	5274														
Thr Cys Lys Tyr His Lys Cys Pro Tyr Ile Ile Gly Thr Thr Asn															
1745	1750	1755													
cag cct gta aaa atg aca ccc aac cat ggc ttt cac ttg agc ttc	5319														
Gln Pro Val Lys Met Thr Pro Asn His Gly Phe His Leu Ser Phe															
1760	1765	1770													
agg atg ttg acc ttc tcc aac aac gtg gag cca gcc aat ggc ttc	5364														

Corrected Sequence Listing2.ST25															
Arg	Met	Leu	Thr	Phe	Ser	Asn	Asn	Val	Glu	Pro	Ala	Asn	Gly	Phe	
1775						1780						1785			
ctg	ggt	cgt	tac	ctg	agg	agg	aag	ctg	gta	gag	tca	gac	agc	gac	5409
Leu	Val	Arg	Tyr	Leu	Arg	Arg	Lys	Leu	Val	Glu	Ser	Asp	Ser	Asp	
1790						1795					1800				
atc	aat	gcc	aac	aag	gaa	gag	ctg	ctt	cgg	gtg	ctc	gac	tgg	gta	5454
Ile	Asn	Ala	Asn	Lys	Glu	Glu	Leu	Leu	Arg	Val	Leu	Asp	Trp	Val	
1805						1810					1815				
ccc	aag	ctg	tgg	tat	cat	ctc	cac	acc	ttc	ctt	gag	aag	cac	agc	5499
Pro	Lys	Leu	Trp	Tyr	His	Leu	His	Thr	Phe	Leu	Glu	Lys	His	Ser	
1820						1825					1830				
acc	tca	gac	ttc	ctc	atc	ggc	cct	tgc	ttc	ttt	ctg	tcg	tgt	ccc	5544
Thr	Ser	Asp	Phe	Leu	Ile	Gly	Pro	Cys	Phe	Phe	Leu	Ser	Cys	Pro	
1835						1840					1845				
att	ggc	att	gag	gac	ttc	cgg	acc	tgg	ttc	att	gac	ctg	tgg	aac	5589
Ile	Gly	Ile	Glu	Asp	Phe	Arg	Thr	Trp	Phe	Ile	Asp	Leu	Trp	Asn	
1850						1855					1860				
aac	tct	atc	att	ccc	tat	cta	cag	gaa	gga	gcc	aag	gat	ggg	ata	5634
Asn	Ser	Ile	Ile	Pro	Tyr	Leu	Gln	Glu	Gly	Ala	Lys	Asp	Gly	Ile	
1865						1870					1875				
aag	gtc	cat	gga	cag	aaa	gct	gct	tgg	gag	gac	cca	gtg	gaa	tgg	5679
Lys	Val	His	Gly	Gln	Lys	Ala	Ala	Trp	Glu	Asp	Pro	Val	Glu	Trp	
1880						1885					1890				
gtc	cgg	gac	aca	ctt	ccc	tgg	cca	tca	gcc	caa	caa	gac	caa	tca	5724
Val	Arg	Asp	Thr	Leu	Pro	Trp	Pro	Ser	Ala	Gln	Gln	Asp	Gln	Ser	
1895						1900					1905				
aag	ctg	tac	cac	ctg	ccc	cca	ccc	acc	gtg	ggc	cct	cac	agc	att	5769
Lys	Leu	Tyr	His	Leu	Pro	Pro	Pro	Thr	Val	Gly	Pro	His	Ser	Ile	
1910						1915					1920				
gcc	tca	cct	ccc	gag	gat	agg	aca	gtc	aaa	gac	agc	acc	cca	agt	5814
Ala	Ser	Pro	Pro	Glu	Asp	Arg	Thr	Val	Lys	Asp	Ser	Thr	Pro	Ser	
1925						1930					1935				
tct	ctg	gac	tca	gat	cct	ctg	atg	gcc	atg	ctg	ctg	aaa	ctt	caa	5859
Ser	Leu	Asp	Ser	Asp	Pro	Leu	Met	Ala	Met	Leu	Leu	Lys	Leu	Gln	
1940						1945					1950				
gaa	gct	gcc	aac	tac	att	gag	tct	cca	gat	cga	gaa	acc	atc	ctg	5904
Glu	Ala	Ala	Asn	Tyr	Ile	Glu	Ser	Pro	Asp	Arg	Glu	Thr	Ile	Leu	
1955						1960					1965				
gac	ccc	aac	ctt	cag	gca	aca	ctt	taagggttcg	gcaatcactg						5948
Asp	Pro	Asn	Leu	Gln	Ala	Thr	Leu								
1970						1975									
tcacccccgg	acagcagaac	gctggcatca	gctatcttag	ctcctcctct	cccctctcct										6008
ctttcagagc	actggctctc	cagccccagg	aggagaacag	gagggaggag	gagatgaaag										6068
aggagggaca	ggttcttggt	gctgtacctt	tgagaacttc	ctaggaagga	atggtggggt										6128
ggcgtttggg	aacttgtgcc	ccctaaacac	atttactggc	ctcctctaata	gactttgggg										6188

Corrected Sequence Listing2.ST25

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aaaagatgat tctgggtctt tcccttgact tcttgtttca attacaaact cctgggcttt 6248
ctggggaggg gttcagaaaa catcaaaaca ctgcagcagt tcctaaatga ttctcacaag 6308
caaccctgag agagacagtc ttgtgagggg gatctggggg aggcaggaag ctctcagat 6368
tttctcacag acccttccca attccatcac cactgccaac aactcctccc ccagagatct 6428
ggctggagcc cagaaaaaga agcatgtggt ttaaaaaatg tttaaataca tctgtaaaag 6488
gtaaaaatga aaaacaaaaa caagcaaaca aacaaaaaac aatggaaaag atgaagctgg 6548
agagagagga accagttgcc aaggtagaga gctgcccgt cctgccctct ggatgacata 6608
ggggacatca acaagacggc tgccaacctg agaagtcacc aaaccacaaa aataacctta 6668
cagccttcag ggaaagacta ccagctctgt ctttctaccc tctaatttaa caatgcataa 6728
gagtcaataa accctacttt tttaaaaaaa aaaaaaaaaag 6768

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<210> 24
<211> 11
<212> PRT
<213> Homo sapiens

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<400> 24

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Arg Gly Ala Ser Ile Leu Pro Leu Thr Asp Phe
1          5          10

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<210> 25
<211> 1976
<212> PRT
<213> Homo sapiens

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<400> 25

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Ile Leu Ile Cys Ile Phe Pro Ala Ala Pro Pro Leu Phe Leu Arg Pro
1          5          10          15

```

```

Arg Pro Ile Ala Pro Arg Leu Pro Cys Ser Phe Leu Phe Pro Gly Phe
          20          25          30

```

```

Leu Pro Arg Val Ser Phe Pro Cys Ala Leu Gly Leu Pro Leu Ser Leu
          35          40          45

```

```

Leu Pro Arg Ser Leu Pro Leu Leu Ser Pro Ser Ser Ser Val Ser Ser
          50          55          60

```

```

Val Leu Ser Leu Pro Leu Leu Leu Pro Arg Leu Leu Leu Arg Ser
65          70          75          80

```

```

Arg Pro Leu Pro Pro Pro Val Pro Ala Asp Ala Arg Ile Val His
          85          90          95

```

Corrected Sequence Listing2.ST25

Ala Leu Leu Ala Gly Arg Met Leu Gly Ser Ser Val Lys Ser Val Gln
100 105 110

Pro Glu Val Glu Leu Ser Ser Gly Gly Gly Asp Glu Gly Ala Asp Glu
115 120 125

Pro Arg Gly Ala Gly Arg Lys Ala Ala Ala Ala Asp Gly Arg Gly Met
130 135 140

Leu Pro Lys Arg Ala Lys Ala Pro Gly Gly Gly Gly Gly Met Ala Lys
145 150 155 160

Ala Ser Ala Ala Glu Leu Lys Val Phe Lys Ser Gly Ser Val Asp Ser
165 170 175

Arg Val Pro Gly Gly Pro Pro Ala Ser Asn Leu Arg Lys Gln Lys Ser
180 185 190

Leu Thr Asn Leu Ser Phe Leu Thr Asp Ser Glu Lys Lys Leu Gln Leu
195 200 205

Tyr Glu Pro Glu Trp Ser Asp Asp Met Ala Lys Ala Pro Lys Gly Leu
210 215 220

Gly Lys Val Gly Ser Lys Gly Arg Glu Ala Pro Leu Met Ser Lys Thr
225 230 235 240

Leu Ser Lys Ser Glu His Ser Leu Phe Gln Ala Lys Gly Ser Pro Ala
245 250 255

Gly Gly Ala Lys Thr Pro Leu Ala Pro Leu Ala Pro Asn Leu Gly Lys
260 265 270

Pro Ser Arg Ile Pro Arg Gly Pro Tyr Ala Glu Val Lys Pro Leu Ser
275 280 285

Lys Ala Pro Glu Ala Ala Val Ser Glu Asp Gly Lys Ser Asp Asp Glu
290 295 300

Leu Leu Ser Ser Lys Ala Lys Ala Gln Lys Ser Ser Gly Pro Val Pro
305 310 315 320

Ser Ala Lys Gly Gln Glu Glu Arg Ala Phe Leu Lys Val Asp Pro Glu
325 330 335

Leu Val Val Thr Val Leu Gly Asp Leu Glu Gln Leu Leu Phe Ser Gln
340 345 350

Corrected Sequence Listing2.ST25

Met Leu Asp Pro Glu Ser Gln Arg Lys Arg Thr Val Gln Asn Val Leu
355 360 365

Asp Leu Arg Gln Asn Leu Glu Glu Thr Met Ser Ser Leu Arg Gly Ser
370 375 380

Gln Val Thr His Ser Ser Leu Glu Met Thr Cys Tyr Asp Ser Asp Asp
385 390 395 400

Ala Asn Pro Arg Ser Val Ser Ser Leu Ser Asn Arg Ser Tyr Pro Leu
405 410 415

Ser Trp Arg Tyr Gly Gln Ser Ser Pro Arg Leu Gln Ala Gly Asp Ala
420 425 430

Pro Ser Val Gly Gly Ser Cys Arg Ser Glu Gly Thr Pro Ala Trp Tyr
435 440 445

Met His Gly Glu Arg Ala His Tyr Ser His Thr Met Pro Met Arg Ser
450 455 460

Pro Ser Lys Leu Ser His Ile Ser Arg Leu Glu Leu Val Glu Ser Leu
465 470 475 480

Asp Ser Asp Glu Val Asp Leu Lys Ser Gly Tyr Met Ser Asp Ser Asp
485 490 495

Leu Met Gly Lys Thr Met Thr Glu Asp Asp Asp Ile Thr Thr Gly Trp
500 505 510

Asp Glu Ser Ser Ser Ile Ser Ser Gly Leu Ser Asp Ala Ser Asp Asn
515 520 525

Leu Ser Ser Glu Glu Phe Asn Ala Ser Ser Ser Leu Asn Ser Leu Pro
530 535 540

Ser Thr Pro Thr Ala Ser Arg Arg Asn Ser Thr Ile Val Leu Arg Thr
545 550 555 560

Asp Ser Glu Lys Arg Ser Leu Ala Glu Ser Gly Leu Ser Trp Phe Ser
565 570 575

Glu Ser Glu Glu Lys Ala Pro Lys Lys Leu Glu Tyr Asp Ser Gly Ser
580 585 590

Leu Lys Met Glu Pro Gly Thr Ser Lys Trp Arg Arg Glu Arg Pro Glu
595 600 605

Corrected Sequence Listing2.ST25

Ser Cys Asp Asp Ser Ser Lys Gly Gly Glu Leu Lys Lys Pro Ile Ser
610 615 620

Leu Gly His Pro Gly Ser Leu Lys Lys Gly Lys Thr Pro Pro Val Ala
625 630 635 640

Val Thr Ser Pro Ile Thr His Thr Ala Gln Ser Ala Leu Lys Val Ala
645 650 655

Gly Lys Pro Glu Gly Lys Ala Thr Asp Lys Gly Lys Leu Ala Val Lys
660 665 670

Asn Thr Gly Leu Gln Arg Ser Ser Ser Asp Ala Gly Arg Asp Arg Leu
675 680 685

Ser Asp Ala Lys Lys Pro Pro Ser Gly Ile Ala Arg Pro Ser Thr Ser
690 695 700

Gly Ser Phe Gly Tyr Lys Lys Pro Pro Pro Ala Thr Gly Thr Ala Thr
705 710 715 720

Val Met Gln Thr Gly Gly Ser Ala Thr Leu Ser Lys Ile Gln Lys Ser
725 730 735

Ser Gly Ile Pro Val Lys Pro Val Asn Gly Arg Lys Thr Ser Leu Asp
740 745 750

Val Ser Asn Ser Ala Glu Pro Gly Phe Leu Ala Pro Gly Ala Arg Ser
755 760 765

Asn Ile Gln Tyr Arg Ser Leu Pro Arg Pro Ala Lys Ser Ser Ser Met
770 775 780

Ser Val Thr Gly Gly Arg Gly Gly Pro Arg Pro Val Ser Ser Ser Ile
785 790 795 800

Asp Pro Ser Leu Leu Ser Thr Lys Gln Gly Gly Leu Thr Pro Ser Arg
805 810 815

Leu Lys Glu Pro Thr Lys Val Ala Ser Gly Arg Thr Thr Pro Ala Pro
820 825 830

Val Asn Gln Thr Asp Arg Glu Lys Glu Lys Ala Lys Ala Lys Ala Val
835 840 845

Ala Leu Asp Ser Asp Asn Ile Ser Leu Lys Ser Ile Gly Ser Pro Glu
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850		855		860	
Ser	Thr	Pro	Lys	Asn	Gln
865				870	Ala
	Ser	His	Pro	Thr	Ala
				875	Thr
					Lys
					Leu
					Ala
					880
Glu	Leu	Pro	Pro	Thr	Pro
				885	Leu
					Arg
					Ala
					Thr
					Ala
					Lys
					Ser
					Phe
					Val
					Lys
					895
Pro	Pro	Ser	Leu	Ala	Asn
			900		Leu
					Asp
					Lys
					Val
					Asn
					Ser
					Asn
					Ser
					Leu
					Asp
					910
Leu	Pro	Ser	Ser	Ser	Asp
		915			Thr
					Thr
					His
					Ala
					Ser
					Lys
					Val
					Pro
					Asp
					Leu
					925
His	Ala	Thr	Ser	Ser	Ala
	930				Ser
					Gly
					Gly
					Pro
					Leu
					Pro
					Ser
					Cys
					Phe
					Thr
					940
Pro	Ser	Pro	Ala	Pro	Ile
945					Leu
					Asn
					Ile
					Asn
					Ser
					Ala
					Ser
					Phe
					Ser
					Gln
					960
Gly	Leu	Glu	Leu	Met	Ser
				965	Gly
					Phe
					Ser
					Val
					Pro
					Lys
					Glu
					Thr
					Arg
					Met
					975
Tyr	Pro	Lys	Leu	Ser	Gly
			980		Leu
					His
					Arg
					Ser
					Met
					Glu
					Ser
					Leu
					Gln
					Met
					990
Pro	Met	Ser	Leu	Pro	Ser
			995		Ala
					Phe
					Pro
					Ser
					Ser
					Thr
					Pro
					Val
					Pro
					Thr
					1000
Pro	Pro	Ala	Pro	Pro	Ala
	1010				Ala
					Pro
					Thr
					Glu
					Glu
					Glu
					Thr
					Glu
					Glu
					1020
Leu	Thr	Trp	Ser	Gly	Ser
	1025				Pro
					Arg
					Ala
					Gly
					Gln
					Leu
					Asp
					Ser
					Asn
					1035
Gln	Arg	Asp	Arg	Asn	Thr
	1040				Leu
					Pro
					Lys
					Lys
					Gly
					Leu
					Arg
					Tyr
					Gln
					1050
Leu	Gln	Ser	Gln	Glu	Glu
	1055				Thr
					Lys
					Glu
					Arg
					Arg
					His
					Ser
					His
					Thr
					1065
Ile	Gly	Gly	Leu	Pro	Glu
	1070				Ser
					Asp
					Asp
					Gln
					Ser
					Glu
					Leu
					Pro
					Ser
					1080
Pro	Pro	Ala	Leu	Pro	Met
					Ser
					Leu
					Ser
					Ala
					Lys
					Gly
					Gln
					Leu
					Thr
					1095
					1085

Corrected Sequence Listing2.ST25

Asn	Ile	Val	Ser	Pro	Thr	Ala	Ala	Thr	Thr	Pro	Arg	Ile	Thr	Arg
1100						1105					1110			
Ser	Asn	Ser	Ile	Pro	Thr	His	Glu	Ala	Ala	Phe	Glu	Leu	Tyr	Ser
1115						1120					1125			
Gly	Ser	Gln	Met	Gly	Ser	Thr	Leu	Ser	Leu	Ala	Glu	Arg	Pro	Lys
1130						1135					1140			
Gly	Met	Ile	Arg	Ser	Gly	Ser	Phe	Arg	Asp	Pro	Thr	Asp	Asp	Val
1145						1150					1155			
His	Gly	Ser	Val	Leu	Ser	Leu	Ala	Ser	Ser	Ala	Ser	Ser	Thr	Tyr
1160						1165					1170			
Ser	Ser	Ala	Glu	Glu	Arg	Met	Gln	Ser	Glu	Gln	Ile	Arg	Lys	Leu
1175						1180					1185			
Arg	Arg	Glu	Leu	Glu	Ser	Ser	Gln	Glu	Lys	Val	Ala	Thr	Leu	Thr
1190						1195					1200			
Ser	Gln	Leu	Ser	Ala	Asn	Ala	Asn	Leu	Val	Ala	Ala	Phe	Glu	Gln
1205						1210					1215			
Ser	Leu	Val	Asn	Met	Thr	Ser	Arg	Leu	Arg	His	Leu	Ala	Glu	Thr
1220						1225					1230			
Ala	Glu	Glu	Lys	Asp	Thr	Glu	Leu	Leu	Asp	Leu	Arg	Glu	Thr	Ile
1235						1240					1245			
Asp	Phe	Leu	Lys	Lys	Lys	Asn	Ser	Glu	Ala	Gln	Ala	Val	Ile	Gln
1250						1255					1260			
Gly	Ala	Leu	Asn	Ala	Ser	Glu	Thr	Thr	Pro	Lys	Glu	Leu	Arg	Ile
1265						1270					1275			
Lys	Arg	Gln	Asn	Ser	Ser	Asp	Ser	Ile	Ser	Ser	Leu	Asn	Ser	Ile
1280						1285					1290			
Thr	Ser	His	Ser	Ser	Ile	Gly	Ser	Ser	Lys	Asp	Ala	Asp	Ala	Lys
1295						1300					1305			
Lys	Lys	Lys	Lys	Lys	Ser	Trp	Leu	Arg	Ser	Ser	Phe	Asn	Lys	Ala
1310						1315					1320			
Phe	Ser	Ile	Lys	Lys	Gly	Pro	Lys	Ser	Ala	Ser	Ser	Tyr	Ser	Asp
1325						1330					1335			

Corrected Sequence Listing2.ST25

Ile	Glu	Glu	Ile	Ala	Thr	Pro	Asp	Ser	Ser	Ala	Pro	Ser	Ser	Pro
1340						1345					1350			
Lys	Leu	Gln	His	Gly	Ser	Thr	Glu	Thr	Ala	Ser	Pro	Ser	Ile	Lys
1355						1360					1365			
Ser	Ser	Thr	Ser	Ser	Ser	Val	Gly	Thr	Asp	Val	Thr	Glu	Gly	Pro
1370						1375					1380			
Ala	His	Pro	Ala	Pro	His	Thr	Arg	Leu	Phe	His	Ala	Asn	Glu	Glu
1385						1390					1395			
Glu	Glu	Pro	Glu	Lys	Lys	Glu	Val	Ser	Glu	Leu	Arg	Ser	Glu	Leu
1400						1405					1410			
Trp	Glu	Lys	Glu	Met	Lys	Leu	Thr	Asp	Ile	Arg	Leu	Glu	Ala	Leu
1415						1420					1425			
Asn	Ser	Ala	His	Gln	Leu	Asp	Gln	Leu	Arg	Glu	Thr	Met	His	Asn
1430						1435					1440			
Met	Gln	Leu	Glu	Val	Asp	Leu	Leu	Glu	Ala	Glu	Asn	Asp	Arg	Leu
1445						1450					1455			
Lys	Val	Ala	Pro	Gly	Pro	Ser	Ser	Gly	Ser	Thr	Pro	Gly	Gln	Val
1460						1465					1470			
Pro	Gly	Ser	Ser	Ala	Leu	Ser	Ser	Pro	Arg	Arg	Ser	Leu	Gly	Leu
1475						1480					1485			
Ala	Leu	Thr	His	Ser	Phe	Gly	Pro	Ser	Leu	Ala	Asp	Thr	Asp	Leu
1490						1495					1500			
Ser	Pro	Met	Asp	Gly	Ile	Ser	Thr	Cys	Gly	Pro	Lys	Glu	Glu	Val
1505						1510					1515			
Thr	Leu	Arg	Val	Val	Val	Arg	Met	Pro	Pro	Gln	His	Ile	Ile	Lys
1520						1525					1530			
Gly	Asp	Leu	Lys	Gln	Gln	Glu	Phe	Phe	Leu	Gly	Cys	Ser	Lys	Val
1535						1540					1545			
Ser	Gly	Lys	Val	Asp	Trp	Lys	Met	Leu	Asp	Glu	Ala	Val	Phe	Gln
1550						1555					1560			
Val	Phe	Lys	Asp	Tyr	Ile	Ser	Lys	Met	Asp	Pro	Ala	Ser	Thr	Leu
1565						1570					1575			

Corrected Sequence Listing2.ST25

Gly	Leu	Ser	Thr	Glu	Ser	Ile	His	Gly	Tyr	Ser	Ile	Ser	His	Val
1580						1585					1590			
Lys	Arg	Val	Leu	Asp	Ala	Glu	Pro	Pro	Glu	Met	Pro	Pro	Cys	Arg
1595						1600					1605			
Arg	Gly	Val	Asn	Asn	Ile	Ser	Val	Ser	Leu	Lys	Gly	Leu	Lys	Glu
1610						1615					1620			
Lys	Cys	Val	Asp	Ser	Leu	Val	Phe	Glu	Thr	Leu	Ile	Pro	Lys	Pro
1625						1630					1635			
Met	Met	Gln	His	Tyr	Ile	Ser	Leu	Leu	Leu	Lys	His	Arg	Arg	Leu
1640						1645					1650			
Val	Leu	Ser	Gly	Pro	Ser	Gly	Thr	Gly	Lys	Thr	Tyr	Leu	Thr	Asn
1655						1660					1665			
Arg	Leu	Ala	Glu	Tyr	Leu	Val	Glu	Arg	Ser	Gly	Arg	Glu	Val	Thr
1670						1675					1680			
Glu	Gly	Ile	Val	Ser	Thr	Phe	Asn	Met	His	Gln	Gln	Ser	Cys	Lys
1685						1690					1695			
Asp	Leu	Gln	Leu	Tyr	Leu	Ser	Asn	Leu	Ala	Asn	Gln	Ile	Asp	Arg
1700						1705					1710			
Glu	Thr	Gly	Ile	Gly	Asp	Val	Pro	Leu	Val	Ile	Leu	Leu	Asp	Asp
1715						1720					1725			
Leu	Ser	Glu	Ala	Gly	Ser	Ile	Ser	Glu	Leu	Val	Asn	Gly	Ala	Leu
1730						1735					1740			
Thr	Cys	Lys	Tyr	His	Lys	Cys	Pro	Tyr	Ile	Ile	Gly	Thr	Thr	Asn
1745						1750					1755			
Gln	Pro	Val	Lys	Met	Thr	Pro	Asn	His	Gly	Phe	His	Leu	Ser	Phe
1760						1765					1770			
Arg	Met	Leu	Thr	Phe	Ser	Asn	Asn	Val	Glu	Pro	Ala	Asn	Gly	Phe
1775						1780					1785			
Leu	Val	Arg	Tyr	Leu	Arg	Arg	Lys	Leu	Val	Glu	Ser	Asp	Ser	Asp
1790						1795					1800			
Ile	Asn	Ala	Asn	Lys	Glu	Glu	Leu	Leu	Arg	Val	Leu	Asp	Trp	Val

Corrected Sequence Listing2.ST25

1805
 1810
 1815
 Pro Lys Leu Trp Tyr His Leu His Thr Phe Leu Glu Lys His Ser
 1820 1825 1830
 Thr Ser Asp Phe Leu Ile Gly Pro Cys Phe Phe Leu Ser Cys Pro
 1835 1840 1845
 Ile Gly Ile Glu Asp Phe Arg Thr Trp Phe Ile Asp Leu Trp Asn
 1850 1855 1860
 Asn Ser Ile Ile Pro Tyr Leu Gln Glu Gly Ala Lys Asp Gly Ile
 1865 1870 1875
 Lys Val His Gly Gln Lys Ala Ala Trp Glu Asp Pro Val Glu Trp
 1880 1885 1890
 Val Arg Asp Thr Leu Pro Trp Pro Ser Ala Gln Gln Asp Gln Ser
 1895 1900 1905
 Lys Leu Tyr His Leu Pro Pro Pro Thr Val Gly Pro His Ser Ile
 1910 1915 1920
 Ala Ser Pro Pro Glu Asp Arg Thr Val Lys Asp Ser Thr Pro Ser
 1925 1930 1935
 Ser Leu Asp Ser Asp Pro Leu Met Ala Met Leu Leu Lys Leu Gln
 1940 1945 1950
 Glu Ala Ala Asn Tyr Ile Glu Ser Pro Asp Arg Glu Thr Ile Leu
 1955 1960 1965
 Asp Pro Asn Leu Gln Ala Thr Leu
 1970 1975

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 Asn Gln Pro Glu Arg Leu Asn Ser Gln Val Leu Gln Gly Leu Gln Glu
 1 5 10 15
 cca gcg ggg gag ggg ctc ccg ctg cgg aag agc ggc tcg gtg gaa aac 97
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Pro	Ala	Gly	Glu	Gly	Leu	Pro	Leu	Arg	Lys	Ser	Gly	Ser	Val	Glu	Asn	
			20					25					30			
ggg	ttc	gat	acc	cag	atc	tac	aca	gac	tgg	gcc	aat	cat	tac	cta	gcc	145
Gly	Phe	Asp	Thr	Gln	Ile	Tyr	Thr	Asp	Trp	Ala	Asn	His	Tyr	Leu	Ala	
		35				40						45				
aaa	tcc	ggc	cac	aag	cgt	ctc	atc	agg	gat	ctc	cag	caa	gat	gtg	aca	193
Lys	Ser	Gly	His	Lys	Arg	Leu	Ile	Arg	Asp	Leu	Gln	Gln	Asp	Val	Thr	
	50				55					60						
gat	ggc	gtc	ctc	ctg	gcc	cag	att	atc	cag	gtt	gtg	gca	aat	gaa	aag	241
Asp	Gly	Val	Leu	Leu	Ala	Gln	Ile	Ile	Gln	Val	Val	Ala	Asn	Glu	Lys	
65				70					75					80		
att	gaa	gac	atc	aat	ggc	tgt	ccg	aag	aac	aga	tcc	caa	atg	att	gaa	289
Ile	Glu	Asp	Ile	Asn	Gly	Cys	Pro	Lys	Asn	Arg	Ser	Gln	Met	Ile	Glu	
			85					90					95			
aac	ata	gat	gcc	tgc	ttg	aat	ttc	ctg	gca	gct	aag	gga	ata	aac	atc	337
Asn	Ile	Asp	Ala	Cys	Leu	Asn	Phe	Leu	Ala	Ala	Lys	Gly	Ile	Asn	Ile	
			100					105					110			
cag	ggg	ctg	tct	gca	gaa	gag	atc	agg	aat	gga	aac	ctc	aag	gcc	att	385
Gln	Gly	Leu	Ser	Ala	Glu	Glu	Ile	Arg	Asn	Gly	Asn	Leu	Lys	Ala	Ile	
		115					120					125				
cta	ggc	ctc	ttc	ttc	agc	ctc	tcc	cga	tac	aag	cag	cag	cag	cag	cag	433
Leu	Gly	Leu	Phe	Phe	Ser	Leu	Ser	Arg	Tyr	Lys	Gln	Gln	Gln	Gln	Gln	
	130					135					140					
ccc	cag	aag	cag	cac	ctc	tcc	tca	cct	ctg	ccg	ccc	gcc	gta	tcc	cag	481
Pro	Gln	Lys	Gln	His	Leu	Ser	Ser	Pro	Leu	Pro	Pro	Ala	Val	Ser	Gln	
145					150				155					160		
gtg	gcc	ggg	gcc	ccc	tcc	cag	tgc	cag	gct	ggc	acc	cct	cag	cag	cag	529
Val	Ala	Gly	Ala	Pro	Ser	Gln	Cys	Gln	Ala	Gly	Thr	Pro	Gln	Gln	Gln	
				165				170					175			
gtg	cca	gtc	act	ccc	caa	gcc	ccg	tgc	cag	cct	cac	cag	cca	gcg	cca	577
Val	Pro	Val	Thr	Pro	Gln	Ala	Pro	Cys	Gln	Pro	His	Gln	Pro	Ala	Pro	
			180					185					190			
cat	cag	cag	tca	aaa	gca	caa	gct	gaa	atg	cag	tcc	aga	ctt	cca	ggt	625
His	Gln	Gln	Ser	Lys	Ala	Gln	Ala	Glu	Met	Gln	Ser	Arg	Leu	Pro	Gly	
		195					200					205				
cct	acc	gcg	agg	gta	tcc	gct	gca	ggc	agc	gag	gcc	aaa	aca	cgc	gga	673
Pro	Thr	Ala	Arg	Val	Ser	Ala	Ala	Gly	Ser	Glu	Ala	Lys	Thr	Arg	Gly	
	210					215					220					
ggg	tca	act	act	gct	aac	aac	cga	cgc	agc	cag	agc	ttt	aac	aac	tat	721
Gly	Ser	Thr	Thr	Ala	Asn	Asn	Arg	Arg	Ser	Gln	Ser	Phe	Asn	Asn	Tyr	
225					230					235					240	
gat	aaa	tcc	aaa	cca	gtc	acc	tcc	cca	ccc	cca	ccg	cca	agc	agc	cac	769
Asp	Lys	Ser	Lys	Pro	Val	Thr	Ser	Pro	Pro	Pro	Pro	Pro	Ser	Ser	His	
				245					250				255			
gag	aaa	gag	cct	ttg	gca	agt	tca	gcc	tcc	tcc	cac	ccc	gga	atg	agt	817
Glu	Lys	Glu	Pro	Leu	Ala	Ser	Ser	Ala	Ser	Ser	His	Pro	Gly	Met	Ser	
			260					265					270			

Corrected Sequence Listing2.ST25																
gac	aat	gca	cct	gct	tcc	ttg	gag	agc	ggc	agc	agc	tcc	acc	cct	act	865
Asp	Asn	Ala	Pro	Ala	Ser	Leu	Glu	Ser	Gly	Ser	Ser	Ser	Thr	Pro	Thr	
		275					280					285				
aat	tgc	agt	acc	tcc	tcg	gcc	atc	ccg	cag	ccc	ggg	gca	gcc	acc	aag	913
Asn	Cys	Ser	Thr	Ser	Ser	Ala	Ile	Pro	Gln	Pro	Gly	Ala	Ala	Thr	Lys	
	290					295					300					
cct	tgg	cgc	agc	aaa	tcc	ctc	agc	gtg	aag	cac	agt	gcc	acg	gta	tcc	961
Pro	Trp	Arg	Ser	Lys	Ser	Leu	Ser	Val	Lys	His	Ser	Ala	Thr	Val	Ser	
305					310					315					320	
atg	ctc	tcg	gtc	aag	cct	cct	ggg	cct	gag	gcc	ccc	agg	ccc	aca	cct	1009
Met	Leu	Ser	Val	Lys	Pro	Pro	Gly	Pro	Glu	Ala	Pro	Arg	Pro	Thr	Pro	
				325					330					335		
gaa	gcc	atg	aag	ccg	gcc	ccc	aac	aat	cag	aag	tcc	atg	ctg	gaa	aag	1057
Glu	Ala	Met	Lys	Pro	Ala	Pro	Asn	Asn	Gln	Lys	Ser	Met	Leu	Glu	Lys	
			340				345						350			
ctg	aaa	ctt	ttc	aac	agt	aaa	ggg	ggc	tca	aag	gca	ggg	gag	ggg	ccg	1105
Leu	Lys	Leu	Phe	Asn	Ser	Lys	Gly	Gly	Ser	Lys	Ala	Gly	Glu	Gly	Pro	
		355					360					365				
ggg	tcc	cgg	gac	aca	agc	tgt	gag	cgg	ctg	gag	act	ctg	ccc	agc	ttc	1153
Gly	Ser	Arg	Asp	Thr	Ser	Cys	Glu	Arg	Leu	Glu	Thr	Leu	Pro	Ser	Phe	
	370					375					380					
gaa	gag	agc	gag	gag	ctg	gag	gcc	gcc	agt	cgc	atg	ctc	acc	acc	gtg	1201
Glu	Glu	Ser	Glu	Glu	Leu	Glu	Ala	Ala	Ser	Arg	Met	Leu	Thr	Thr	Val	
385					390					395					400	
ggc	cct	gct	tcc	agc	agc	ccc	aag	att	gca	ctc	aag	ggc	att	gcc	cag	1249
Gly	Pro	Ala	Ser	Ser	Ser	Pro	Lys	Ile	Ala	Leu	Lys	Gly	Ile	Ala	Gln	
				405					410					415		
agg	act	ttt	agc	cgg	gca	ctg	acc	aac	aag	aag	agt	tct	ctg	aaa	ggc	1297
Arg	Thr	Phe	Ser	Arg	Ala	Leu	Thr	Asn	Lys	Lys	Ser	Ser	Leu	Lys	Gly	
			420					425					430			
aat	gag	aaa	gag	aag	gag	aaa	caa	cag	cgg	gag	aag	gat	aag	gag	aaa	1345
Asn	Glu	Lys	Glu	Lys	Glu	Lys	Gln	Gln	Arg	Glu	Lys	Asp	Lys	Glu	Lys	
		435					440					445				
agc	aag	gac	ctt	gcc	aag	aga	gcc	tct	gtg	acg	gag	agg	ctg	gac	ctc	1393
Ser	Lys	Asp	Leu	Ala	Lys	Arg	Ala	Ser	Val	Thr	Glu	Arg	Leu	Asp	Leu	
	450					455					460					
aag	gag	gag	cca	aaa	gaa	gac	ccc	agt	gga	gca	gct	gtg	ccc	gag	atg	1441
Lys	Glu	Glu	Pro	Lys	Glu	Asp	Pro	Ser	Gly	Ala	Ala	Val	Pro	Glu	Met	
465					470				475						480	
cca	aaa	aag	tcc	tcc	aag	att	gcc	agc	ttc	atc	ccc	aaa	ggg	ggg	aag	1489
Pro	Lys	Lys	Ser	Ser	Lys	Ile	Ala	Ser	Phe	Ile	Pro	Lys	Gly	Gly	Lys	
				485					490				495			
ctc	aac	agt	gcc	aag	aag	gag	ccc	atg	gcc	cct	tcc	cac	agt	gga	ata	1537
Leu	Asn	Ser	Ala	Lys	Lys	Glu	Pro	Met	Ala	Pro	Ser	His	Ser	Gly	Ile	
			500					505					510			
cca	aaa	cca	gga	atg	aag	agc	atg	ccc	ggg	aaa	tcc	cca	agt	gcc	cca	1585
Pro	Lys	Pro	Gly	Met	Lys	Ser	Met	Pro	Gly	Lys	Ser	Pro	Ser	Ala	Pro	
		515					520					525				

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gcg cct tcc aag gaa ggg gag cgg agc cgg agt ggg aag ctg agc tca Ala Pro Ser Lys Glu Gly Glu Arg Ser Arg Ser Gly Lys Leu Ser Ser 530 535 540	1633
gga ctc ccc cag cag aag ccc cag ctg gac ggc aga cac tcc agt tcc Gly Leu Pro Gln Gln Lys Pro Gln Leu Asp Gly Arg His Ser Ser Ser 545 550 555 560	1681
tct tcc agc ctg gcg tcc tca gaa gga aaa ggc cca gga ggg acc acc Ser Ser Ser Leu Ala Ser Ser Glu Gly Lys Gly Pro Gly Gly Thr Thr 565 570 575	1729
ctg aac cac agc atc agc agc cag act gtc agt ggg tct gtc ggg acc Leu Asn His Ser Ile Ser Ser Gln Thr Val Ser Gly Ser Val Gly Thr 580 585 590	1777
acc cag acc aca gga agc aat acc gtc agt gtt cag cta cct cag ccc Thr Gln Thr Thr Gly Ser Asn Thr Val Ser Val Gln Leu Pro Gln Pro 595 600 605	1825
cag cag caa tac aac cat ccc aac act gcc acg gtt gca cct ttc ctg Gln Gln Gln Tyr Asn His Pro Asn Thr Ala Thr Val Ala Pro Phe Leu 610 615 620	1873
tac agg tct cag acg gac act gaa ggg aat gtt act gcc gag tca agc Tyr Arg Ser Gln Thr Asp Thr Glu Gly Asn Val Thr Ala Glu Ser Ser 625 630 635 640	1921
tca aca ggt gtg agc gtg gag ccc agc cac ttc acc aag act gga cag Ser Thr Gly Val Ser Val Glu Pro Ser His Phe Thr Lys Thr Gly Gln 645 650 655	1969
cct gct ctg gaa gaa ctc act ggg gaa gat cct gag gct cgg cgg ctg Pro Ala Leu Glu Glu Leu Thr Gly Glu Asp Pro Glu Ala Arg Arg Leu 660 665 670	2017
cgg aca gtg aag aac atc gct gat ctg cgg cag aat ttg gag gaa acc Arg Thr Val Lys Asn Ile Ala Asp Leu Arg Gln Asn Leu Glu Glu Thr 675 680 685	2065
atg tcc agt tta agg gga act cag gtt aca cac agc aca ttg gaa acc Met Ser Ser Leu Arg Gly Thr Gln Val Thr His Ser Thr Leu Glu Thr 690 695 700	2113
acg ttt gac acc aat gtc acc acg gag atg agt ggc cgt agc ata ctc Thr Phe Asp Thr Asn Val Thr Thr Glu Met Ser Gly Arg Ser Ile Leu 705 710 715 720	2161
agc ttg aca ggg agg ccc aca cct ctg tcc tgg aga ctg ggc cag tcc Ser Leu Thr Gly Arg Pro Thr Pro Leu Ser Trp Arg Leu Gly Gln Ser 725 730 735	2209
agc cct cgg ctc caa gca gga gac gcc ccc tca atg ggc aat ggg tat Ser Pro Arg Leu Gln Ala Gly Asp Ala Pro Ser Met Gly Asn Gly Tyr 740 745 750	2257
ccc cct cga gcc aac gcc agc agg ttc atc aac act gag tca ggt cgc Pro Pro Arg Ala Asn Ala Ser Arg Phe Ile Asn Thr Glu Ser Gly Arg 755 760 765	2305
tat gtg tac tcc gcc cct ctg aga agg cag ctg gcc tcc cgg ggc agt Tyr Val Tyr Ser Ala Pro Leu Arg Arg Gln Leu Ala Ser Arg Gly Ser 770 775 780 785	2353

Corrected Sequence Listing2.ST25

770	775	780	
agt gtc tgc cac gtg gac gtc tca gac aag gca gga gat gag atg gac Ser Val Cys His Val Asp Val Ser Asp Lys Ala Gly Asp Glu Met Asp 785 790 795 800			2401
ctg gaa ggc atc agc atg gac gcc ccc ggc tac atg agc gat ggg gat Leu Glu Gly Ile Ser Met Asp Ala Pro Gly Tyr Met Ser Asp Gly Asp 805 810 815			2449
gtt ctg agc aag aac atc cgg acc gat gac att aca agc gga tac atg Val Leu Ser Lys Asn Ile Arg Thr Asp Asp Ile Thr Ser Gly Tyr Met 820 825 830			2497
act gat ggt gga ctt ggc ctc tat acc cgt cgc ctg aac cgg ctc cct Thr Asp Gly Gly Leu Gly Leu Tyr Thr Arg Arg Leu Asn Arg Leu Pro 835 840 845			2545
gat ggg atg gct gtg gta cgg gag acc ctg caa cga aat acc tcc ctg Asp Gly Met Ala Val Val Arg Glu Thr Leu Gln Arg Asn Thr Ser Leu 850 855 860			2593
ggc ctc gga gac gct gac agc tgg gac gac agc agc tcc gtc agc agc Gly Leu Gly Asp Ala Asp Ser Trp Asp Asp Ser Ser Val Ser Ser 865 870 875 880			2641
ggc atc agc gac acc ata gac aac ctc agc act gat gac atc aac acc Gly Ile Ser Asp Thr Ile Asp Asn Leu Ser Thr Asp Asp Ile Asn Thr 885 890 895			2689
agc tcc tcc atc agc tct tat gcc aac aca cct gcc tcc tct cga aaa Ser Ser Ser Ile Ser Ser Tyr Ala Asn Thr Pro Ala Ser Ser Arg Lys 900 905 910			2737
aac ctg gat gtg cag act gat gct gag aag cac tca cag gtg gag agg Asn Leu Asp Val Gln Thr Asp Ala Glu Lys His Ser Gln Val Glu Arg 915 920 925			2785
aat tcc ctg tgg tct ggt gat gat gtc aag aaa tca gac gga ggc tca Asn Ser Leu Trp Ser Gly Asp Asp Val Lys Lys Ser Asp Gly Gly Ser 930 935 940			2833
gac agc ggc ata aaa atg gag cca ggt tcc aag tgg agg cgg aat cct Asp Ser Gly Ile Lys Met Glu Pro Gly Ser Lys Trp Arg Arg Asn Pro 945 950 955 960			2881
tct gat gtg tct gac gag tcc gac aaa agc acg tcg ggc aag aag aat Ser Asp Val Ser Asp Glu Ser Asp Lys Ser Thr Ser Gly Lys Lys Asn 965 970 975			2929
cct gtc atc tcc cag aca ggc tca tgg cgg cga ggc atg aca gct cag Pro Val Ile Ser Gln Thr Gly Ser Trp Arg Arg Gly Met Thr Ala Gln 980 985 990			2977
gtg ggc atc acc atg cca agg acg aag gct tca gcc ccg gca ggc gca Val Gly Ile Thr Met Pro Arg Thr Lys Ala Ser Ala Pro Ala Gly Ala 995 1000 1005			3025
ctg aag acc cca gga act gga aaa aca gac gac gca aag gtg tct Leu Lys Thr Pro Gly Thr Gly Lys Thr Asp Asp Ala Lys Val Ser 1010 1015 1020			3070
gag aaa gga agg ctt tct cct aaa gcc tcc cag gtg aag cgc tcc			3115

Corrected Sequence Listing2.ST25															
Glu	Lys	Gly	Arg	Leu	Ser	Pro	Lys	Ala	Ser	Gln	Val	Lys	Arg	Ser	
1025						1030					1035				
cca	tca	gat	gca	ggc	cgg	agc	agt	ggt	gac	gaa	tcc	aaa	aag	ccc	3160
Pro	Ser	Asp	Ala	Gly	Arg	Ser	Ser	Gly	Asp	Glu	Ser	Lys	Lys	Pro	
1040						1045					1050				
ctc	ccc	agc	agc	tct	agg	aca	cct	act	gcc	aat	gcc	aac	agc	ttt	3205
Leu	Pro	Ser	Ser	Ser	Arg	Thr	Pro	Thr	Ala	Asn	Ala	Asn	Ser	Phe	
1055						1060					1065				
ggg	ttc	aag	aag	cag	agt	ggt	tcc	gcc	acc	ggc	ctg	gcc	atg	atc	3250
Gly	Phe	Lys	Lys	Gln	Ser	Gly	Ser	Ala	Thr	Gly	Leu	Ala	Met	Ile	
1070						1075					1080				
aca	gcc	agc	ggg	gtg	act	gtc	acc	agc	agg	tca	gcc	aca	ctg	ggc	3295
Thr	Ala	Ser	Gly	Val	Thr	Val	Thr	Ser	Arg	Ser	Ala	Thr	Leu	Gly	
1085						1090					1095				
aaa	atc	cca	aag	tca	tct	gca	ctc	gtc	agt	cgg	tct	gct	ggc	cgg	3340
Lys	Ile	Pro	Lys	Ser	Ser	Ala	Leu	Val	Ser	Arg	Ser	Ala	Gly	Arg	
1100						1105					1110				
aag	tca	agt	atg	gat	ggg	gct	cag	aat	cag	gat	gac	ggg	tat	cta	3385
Lys	Ser	Ser	Met	Asp	Gly	Ala	Gln	Asn	Gln	Asp	Asp	Gly	Tyr	Leu	
1115						1120					1125				
gcc	cta	agc	tcc	cgg	aca	aac	ctt	cag	tac	cgg	agt	ttg	ccg	agg	3430
Ala	Leu	Ser	Ser	Arg	Thr	Asn	Leu	Gln	Tyr	Arg	Ser	Leu	Pro	Arg	
1130						1135					1140				
ccc	agt	aag	tcc	aac	agc	cgg	aac	ggg	gct	ggg	aac	agg	tct	agc	3475
Pro	Ser	Lys	Ser	Asn	Ser	Arg	Asn	Gly	Ala	Gly	Asn	Arg	Ser	Ser	
1145						1150					1155				
acc	agc	agc	ata	gat	tcc	aac	att	agc	agc	aag	tcc	gca	ggc	ctg	3520
Thr	Ser	Ser	Ile	Asp	Ser	Asn	Ile	Ser	Ser	Lys	Ser	Ala	Gly	Leu	
1160						1165					1170				
cca	gtg	ccc	aaa	ctg	agg	gag	cct	tcc	aaa	aca	gcc	cta	ggc	agc	3565
Pro	Val	Pro	Lys	Leu	Arg	Glu	Pro	Ser	Lys	Thr	Ala	Leu	Gly	Ser	
1175						1180					1185				
tct	cta	cca	ggt	ctg	gtc	aac	caa	aca	gac	aag	gag	aaa	ggc	atc	3610
Ser	Leu	Pro	Gly	Leu	Val	Asn	Gln	Thr	Asp	Lys	Glu	Lys	Gly	Ile	
1190						1195					1200				
tca	tca	gac	aac	gag	agt	gtg	gct	tcc	tgt	aac	tcg	gtg	aaa	gtg	3655
Ser	Ser	Asp	Asn	Glu	Ser	Val	Ala	Ser	Cys	Asn	Ser	Val	Lys	Val	
1205						1210					1215				
aat	ccg	gca	gcc	cag	cct	gtg	tcc	agt	ccg	gct	cag	acc	agt	ctc	3700
Asn	Pro	Ala	Ala	Gln	Pro	Val	Ser	Ser	Pro	Ala	Gln	Thr	Ser	Leu	
1220						1225					1230				
cag	cct	gga	gcc	aag	tac	cca	gat	gtg	gcc	tct	ccc	aca	ctc	cgc	3745
Gln	Pro	Gly	Ala	Lys	Tyr	Pro	Asp	Val	Ala	Ser	Pro	Thr	Leu	Arg	
1235						1240					1245				
aga	ctc	ttt	ggt	ggg	aag	cct	acc	aag	caa	gtg	ccc	atc	gcc	aca	3790
Arg	Leu	Phe	Gly	Gly	Lys	Pro	Thr	Lys	Gln	Val	Pro	Ile	Ala	Thr	
1250						1255					1260				

Corrected Sequence Listing2.ST25															
gct Ala 1265	gaa Glu 1265	aac Asn 1265	atg Met 1265	aaa Lys 1265	aat Asn 1265	tcg Ser 1270	gtg Val 1270	gtc Val 1270	atc Ile 1270	tcc Ser 1270	aat Asn 1275	cct Pro 1275	cat His 1275	gcc Ala 1275	3835
acc Thr 1280	atg Met 1280	act Thr 1280	cag Gln 1280	caa Gln 1280	ggg Gly 1285	aac Asn 1285	cta Leu 1285	gac Asp 1285	tcc Ser 1285	ccg Pro 1285	tca Ser 1290	ggc Gly 1290	agt Ser 1290	ggc Gly 1290	3880
gtc Val 1295	ctg Leu 1295	agc Ser 1295	agt Ser 1295	ggg Gly 1295	agc Ser 1300	agc Ser 1300	agt Ser 1300	cct Pro 1300	ctc Leu 1300	tac Tyr 1300	agc Ser 1305	aag Lys 1305	aat Asn 1305	gtg Val 1305	3925
gac Asp 1310	ctc Leu 1310	aac Asn 1310	cag Gln 1310	tct Ser 1310	ccg Pro 1310	cta Leu 1315	gcc Ala 1315	tcc Ser 1315	agc Ser 1315	ccc Pro 1315	agc Ser 1320	tca Ser 1320	gcc Ala 1320	cac His 1320	3970
tcg Ser 1325	gcc Ala 1325	cct Pro 1325	tcc Ser 1325	aac Asn 1325	agc Ser 1325	ctc Leu 1330	acc Thr 1330	tgg Trp 1330	ggc Gly 1330	acc Thr 1330	aac Asn 1335	gcc Ala 1335	agc Ser 1335	agc Ser 1335	4015
tcc Ser 1340	tcc Ser 1340	gca Ala 1340	gtt Val 1340	agc Ser 1340	aag Lys 1340	gat Asp 1345	ggc Gly 1345	ctg Leu 1345	ggc Gly 1345	ttt Phe 1345	cag Gln 1350	tct Ser 1350	gtc Val 1350	agc Ser 1350	4060
agc Ser 1355	ctc Leu 1355	cac His 1355	acc Thr 1355	agc Ser 1355	tgt Cys 1355	gag Glu 1360	tcc Ser 1360	atc Ile 1360	gac Asp 1360	atc Ile 1360	tcc Ser 1365	ctc Leu 1365	agc Ser 1365	agt Ser 1365	4105
gga Gly 1370	ggg Gly 1370	gtc Val 1370	ccc Pro 1370	agc Ser 1370	cac His 1370	aat Asn 1375	tct Ser 1375	tcc Ser 1375	act Thr 1375	ggc Gly 1375	ctc Leu 1380	atc Ile 1380	gcc Ala 1380	tcc Ser 1380	4150
tcc Ser 1385	aag Lys 1385	gac Asp 1385	gac Asp 1385	tcc Ser 1385	ttg Leu 1385	act Thr 1390	ccc Pro 1390	ttt Phe 1390	gtc Val 1390	aga Arg 1390	act Thr 1395	aac Asn 1395	agt Ser 1395	gtg Val 1395	4195
aag Lys 1400	acc Thr 1400	aca Thr 1400	ctg Leu 1400	tca Ser 1400	gaa Glu 1400	agc Ser 1405	cct Pro 1405	ctc Leu 1405	tct Ser 1405	tcc Ser 1405	cct Pro 1410	gct Ala 1410	gct Ala 1410	agc Ser 1410	4240
cct Pro 1415	aag Lys 1415	ttc Phe 1415	tgc Cys 1415	aga Arg 1415	agt Ser 1415	act Thr 1420	ctg Leu 1420	ccc Pro 1420	agg Arg 1420	aaa Lys 1420	cag Gln 1425	gac Asp 1425	agt Ser 1425	gac Asp 1425	4285
ccg Pro 1430	cac His 1430	ctt Leu 1430	gat Asp 1430	agg Arg 1430	aac Asn 1430	act Thr 1435	ttg Leu 1435	cct Pro 1435	aag Lys 1435	aaa Lys 1435	gga Gly 1440	ctc Leu 1440	agg Arg 1440	tat Tyr 1440	4330
act Thr 1445	ccc Pro 1445	acc Thr 1445	tcc Ser 1445	cag Gln 1445	ctt Leu 1445	cgc Arg 1450	acg Thr 1450	caa Gln 1450	gaa Glu 1450	gat Asp 1450	gca Ala 1455	aaa Lys 1455	gaa Glu 1455	tgg Trp 1455	4375
tta Leu 1460	cgg Arg 1460	tcc Ser 1460	cat His 1460	tct Ser 1460	gca Ala 1460	gga Gly 1465	ggc Gly 1465	ctt Leu 1465	cag Gln 1465	gac Asp 1465	acc Thr 1470	gct Ala 1470	gcc Ala 1470	aat Asn 1470	4420
tcc Ser 1475	ccc Pro 1475	ttt Phe 1475	tcc Ser 1475	tct Ser 1475	ggc Gly 1475	tcc Ser 1480	agc Ser 1480	gtg Val 1480	act Thr 1480	tct Ser 1480	ccc Pro 1485	tcc Ser 1485	gga Gly 1485	aca Thr 1485	4465
aga Arg 1490	ttc Phe 1490	aac Asn 1490	ttt Phe 1490	tcc Ser 1490	cag Gln 1490	ctt Leu 1495	gcg Ala 1495	agt Ser 1495	ccc Pro 1495	acc Thr 1495	act Thr 1500	gtc Val 1500	acc Thr 1500	cag Gln 1500	4510

Corrected Sequence Listing2.ST25

atg agc ttg tcc aac ccg acc atg ctg agg act cac agc ctc tcc	4555
Met Ser Leu Ser Asn Pro Thr Met Leu Arg Thr His Ser Leu Ser	
1505 1510 1515	
aat gct gat ggg cag tat gat cca tac act gac agc cgc ttc cgg	4600
Asn Ala Asp Gly Gln Tyr Asp Pro Tyr Thr Asp Ser Arg Phe Arg	
1520 1525 1530	
aat agc tcc atg tcc ctg gat gag aag agc aga acc atg agc cgt	4645
Asn Ser Ser Met Ser Leu Asp Glu Lys Ser Arg Thr Met Ser Arg	
1535 1540 1545	
tca ggc tca ttc cgg gat ggg ttt gaa gaa gtt cat gga tcc tca	4690
Ser Gly Ser Phe Arg Asp Gly Phe Glu Glu Val His Gly Ser Ser	
1550 1555 1560	
ctc tcc ttg gtt tcc agc aca tcg tca gtt tat tct aca cca gaa	4735
Leu Ser Leu Val Ser Ser Thr Ser Ser Val Tyr Ser Thr Pro Glu	
1565 1570 1575	
gaa aaa tgc cag tca gag att cgc aag ctg cgg cgg gaa ctg gat	4780
Glu Lys Cys Gln Ser Glu Ile Arg Lys Leu Arg Arg Glu Leu Asp	
1580 1585 1590	
gcc tcc cag gag aaa gtt tca gct ttg acc acc cag ctg aca gca	4825
Ala Ser Gln Glu Lys Val Ser Ala Leu Thr Thr Gln Leu Thr Ala	
1595 1600 1605	
aat gct cac ctt gtg gct gcc ttt gaa cag agt ctt ggt aac atg	4870
Asn Ala His Leu Val Ala Ala Phe Glu Gln Ser Leu Gly Asn Met	
1610 1615 1620	
aca atc agg ctc cag agt ctg acc atg aca gct gag cag aag gat	4915
Thr Ile Arg Leu Gln Ser Leu Thr Met Thr Ala Glu Gln Lys Asp	
1625 1630 1635	
tca gaa ctg aat gag tta aga aaa acc att gag ctg cta aag aaa	4960
Ser Glu Leu Asn Glu Leu Arg Lys Thr Ile Glu Leu Leu Lys Lys	
1640 1645 1650	
cag aac gca gct gcc cag gct gcc att aat gga gta att aac aca	5005
Gln Asn Ala Ala Ala Gln Ala Ala Ile Asn Gly Val Ile Asn Thr	
1655 1660 1665	
cct gag ctc aac tgc aaa gga aac ggc act gcc cag tct gca gac	5050
Pro Glu Leu Asn Cys Lys Gly Asn Gly Thr Ala Gln Ser Ala Asp	
1670 1675 1680	
ctc cgc atc cgc agg cag cac tcc tca gac agc gtc tcc agc atc	5095
Leu Arg Ile Arg Arg Gln His Ser Ser Asp Ser Val Ser Ser Ile	
1685 1690 1695	
aac agt gcc acc agc cac tcc agt gtg ggc agc aac ata gag agt	5140
Asn Ser Ala Thr Ser His Ser Ser Val Gly Ser Asn Ile Glu Ser	
1700 1705 1710	
gac tca aag aag aag aag agg aag aac tgg gtc aat gag tta cgc	5185
Asp Ser Lys Lys Lys Lys Arg Lys Asn Trp Val Asn Glu Leu Arg	
1715 1720 1725	
agc tcc ttc aag caa gct ttc ggg aag aag aag tcc cca aaa tct	5230
Ser Ser Phe Lys Gln Ala Phe Gly Lys Lys Lys Ser Pro Lys Ser	

Corrected Sequence Listing2.ST25															
1730						1735	1740								
gcg	tcc	tct	cat	tca	gat	att	gag	gag	atg	acg	gat	tct	tct	ttg	5275
Ala	Ser	Ser	His	Ser	Asp	Ile	Glu	Glu	Met	Thr	Asp	Ser	Ser	Leu	
1745						1750	1755								
cct	tcc	tca	cca	aag	tta	cca	cac	aat	ggg	tcc	aca	ggt	tcc	acc	5320
Pro	Ser	Ser	Pro	Lys	Leu	Pro	His	Asn	Gly	Ser	Thr	Gly	Ser	Thr	
1760						1765	1770								
cca	ctg	ctg	agg	aat	tct	cac	tcc	aac	tct	cta	att	tca	gaa	tgc	5365
Pro	Leu	Leu	Arg	Asn	Ser	His	Ser	Asn	Ser	Leu	Ile	Ser	Glu	Cys	
1775						1780	1785								
atg	gat	agt	gaa	gct	gag	acc	gtc	atg	cag	ctc	cga	aat	gag	tta	5410
Met	Asp	Ser	Glu	Ala	Glu	Thr	Val	Met	Gln	Leu	Arg	Asn	Glu	Leu	
1790						1795	1800								
aga	gac	aag	gag	atg	aag	ctg	aca	gat	atc	cgc	tta	gaa	gct	ctc	5455
Arg	Asp	Lys	Glu	Met	Lys	Leu	Thr	Asp	Ile	Arg	Leu	Glu	Ala	Leu	
1805						1810	1815								
agt	tct	gcc	cac	cag	ctg	gac	cag	ctc	cgg	gag	gcc	atg	aac	agg	5500
Ser	Ser	Ala	His	Gln	Leu	Asp	Gln	Leu	Arg	Glu	Ala	Met	Asn	Arg	
1820						1825	1830								
atg	cag	agt	gaa	ata	gag	aag	ctg	aaa	gct	gag	aat	gat	cgg	ctg	5545
Met	Gln	Ser	Glu	Ile	Glu	Lys	Leu	Lys	Ala	Glu	Asn	Asp	Arg	Leu	
1835						1840	1845								
aag	tca	gag	tct	caa	ggc	agt	ggc	tgc	agc	cgg	gct	cct	tcc	caa	5590
Lys	Ser	Glu	Ser	Gln	Gly	Ser	Gly	Cys	Ser	Arg	Ala	Pro	Ser	Gln	
1850						1855	1860								
gtg	tcc	atc	tct	gcc	tcc	ccg	agg	cag	tcc	atg	ggc	ctc	tcc	cag	5635
Val	Ser	Ile	Ser	Ala	Ser	Pro	Arg	Gln	Ser	Met	Gly	Leu	Ser	Gln	
1865						1870	1875								
cac	agc	ttg	aac	ctc	act	gag	tca	acc	agc	ctg	gac	atg	ttg	ctg	5680
His	Ser	Leu	Asn	Leu	Thr	Glu	Ser	Thr	Ser	Leu	Asp	Met	Leu	Leu	
1880						1885	1890								
gat	gac	act	ggt	gaa	tgc	tcg	gct	cgg	aag	gaa	gga	ggc	agg	cat	5725
Asp	Asp	Thr	Gly	Glu	Cys	Ser	Ala	Arg	Lys	Glu	Gly	Gly	Arg	His	
1895						1900	1905								
gtt	aag	ata	gtt	gtc	agc	ttt	cag	gag	gaa	atg	aag	tgg	aag	gag	5770
Val	Lys	Ile	Val	Val	Ser	Phe	Gln	Glu	Glu	Met	Lys	Trp	Lys	Glu	
1910						1915	1920								
gat	tcc	aga	cca	cat	ctc	ttt	ctt	att	ggc	tgc	att	gga	gtt	agt	5815
Asp	Ser	Arg	Pro	His	Leu	Phe	Leu	Ile	Gly	Cys	Ile	Gly	Val	Ser	
1925						1930	1935								
ggc	aag	acg	aag	tgg	gat	gtg	ctc	gat	ggg	gtg	gtt	aga	cgg	ctg	5860
Gly	Lys	Thr	Lys	Trp	Asp	Val	Leu	Asp	Gly	Val	Val	Arg	Arg	Leu	
1940						1945	1950								
ttc	aaa	gaa	tac	atc	att	cat	gtc	gac	cca	gtg	agt	cag	cta	ggg	5905
Phe	Lys	Glu	Tyr	Ile	Ile	His	Val	Asp	Pro	Val	Ser	Gln	Leu	Gly	
1955						1960	1965								
ctg	aat	tca	gac	agc	gtt	ctt	ggc	tac	agc	att	gga	gaa	atc	aag	5950

Corrected Sequence Listing2.ST25															
Leu	Asn	Ser	Asp	Ser	Val	Leu	Gly	Tyr	Ser	Ile	Gly	Glu	Ile	Lys	
1970						1975					1980				
cgc	agc	aac	act	tcc	gaa	aca	ccg	gag	ctg	ctt	cct	tgt	ggc	tat	5995
Arg	Ser	Asn	Thr	Ser	Glu	Thr	Pro	Glu	Leu	Leu	Pro	Cys	Gly	Tyr	
1985						1990					1995				
ctg	gtt	gga	gag	aac	acg	acc	atc	tca	gtg	act	gtg	aaa	ggg	ctc	6040
Leu	Val	Gly	Glu	Asn	Thr	Thr	Ile	Ser	Val	Thr	Val	Lys	Gly	Leu	
2000						2005					2010				
gca	gaa	aac	agc	ctg	gac	tca	ctg	gtg	ttt	gag	tcc	ttg	att	ccc	6085
Ala	Glu	Asn	Ser	Leu	Asp	Ser	Leu	Val	Phe	Glu	Ser	Leu	Ile	Pro	
2015						2020					2025				
aag	ccc	atc	ctg	cag	cgc	tac	gtc	tcc	ctc	ctg	ata	gag	cac	cgt	6130
Lys	Pro	Ile	Leu	Gln	Arg	Tyr	Val	Ser	Leu	Leu	Ile	Glu	His	Arg	
2030						2035					2040				
cgg	atc	att	ctc	tct	ggc	ccc	agc	ggc	act	ggg	aaa	acc	tac	ctg	6175
Arg	Ile	Ile	Leu	Ser	Gly	Pro	Ser	Gly	Thr	Gly	Lys	Thr	Tyr	Leu	
2045						2050					2055				
gcc	aac	cgg	ctg	tct	gag	tat	ata	gtg	ctt	cga	gag	gga	cgg	gag	6220
Ala	Asn	Arg	Leu	Ser	Glu	Tyr	Ile	Val	Leu	Arg	Glu	Gly	Arg	Glu	
2060						2065					2070				
ttg	aca	gac	ggg	gtt	atc	gcc	acc	ttt	aac	gtg	gac	cat	aag	tcc	6265
Leu	Thr	Asp	Gly	Val	Ile	Ala	Thr	Phe	Asn	Val	Asp	His	Lys	Ser	
2075						2080					2085				
agc	aag	gaa	ttg	cgc	cag	tac	ctg	tcc	aac	ctt	gct	gac	cag	tgc	6310
Ser	Lys	Glu	Leu	Arg	Gln	Tyr	Leu	Ser	Asn	Leu	Ala	Asp	Gln	Cys	
2090						2095					2100				
aac	agt	gag	aac	aat	gct	gtg	gac	atg	ccc	ctc	gtc	atc	atc	ctg	6355
Asn	Ser	Glu	Asn	Asn	Ala	Val	Asp	Met	Pro	Leu	Val	Ile	Ile	Leu	
2105						2110					2115				
gac	aac	cta	cac	cac	gtg	agc	tct	ctg	ggc	gag	atc	ttc	aat	ggg	6400
Asp	Asn	Leu	His	His	Val	Ser	Ser	Leu	Gly	Glu	Ile	Phe	Asn	Gly	
2120						2125					2130				
ctg	ctc	aac	tgc	aag	tac	cac	aaa	tgc	cct	tac	ata	att	ggc	aca	6445
Leu	Leu	Asn	Cys	Lys	Tyr	His	Lys	Cys	Pro	Tyr	Ile	Ile	Gly	Thr	
2135						2140					2145				
atg	aac	cag	gct	acc	tct	tcg	act	ccc	aac	ctg	cag	ctt	cac	cat	6490
Met	Asn	Gln	Ala	Thr	Ser	Ser	Thr	Pro	Asn	Leu	Gln	Leu	His	His	
2150						2155					2160				
aac	ttc	aga	tgg	gtg	ctt	tgt	gcc	aac	cac	acg	gag	cct	gtg	aag	6535
Asn	Phe	Arg	Trp	Val	Leu	Cys	Ala	Asn	His	Thr	Glu	Pro	Val	Lys	
2165						2170					2175				
ggg	ttc	ctt	ggc	cga	ttc	ctg	agg	agg	aag	ctc	atg	gaa	aca	gag	6580
Gly	Phe	Leu	Gly	Arg	Phe	Leu	Arg	Arg	Lys	Leu	Met	Glu	Thr	Glu	
2180						2185					2190				
atc	agt	ggg	cgg	gtg	cgc	aat	atg	gag	ctg	gta	aaa	atc	att	gac	6625
Ile	Ser	Gly	Arg	Val	Arg	Asn	Met	Glu	Leu	Val	Lys	Ile	Ile	Asp	
2195						2200					2205				

Corrected Sequence Listing2.ST25														
tgg att ccc aag gtc tgg	cat cac ctc aac cgc ttc	ctg gag gct	6670											
Trp Ile Pro Lys Val Trp	His His Leu Asn Arg Phe	Leu Glu Ala												
2210	2215	2220												
cac agt tcc tcg gac gtc	acc atc ggc ccc cgg ctc	ttc ctg tca	6715											
His Ser Ser Ser Asp Val	Thr Ile Gly Pro Arg Leu	Phe Leu Ser												
2225	2230	2235												
tgc ccc atc gat gtg gac	ggc tcg aga gtg tgg	ttc acc gac ttg	6760											
Cys Pro Ile Asp Val Asp	Gly Ser Arg Val Trp Phe	Thr Asp Leu												
2240	2245	2250												
tgg aac tat tcc att atc	ccc tat ctc ctg gaa gcc	gtc aga gaa	6805											
Trp Asn Tyr Ser Ile Ile	Pro Tyr Leu Leu Glu Ala	Val Arg Glu												
2255	2260	2265												
gga ctc cag ctc tat gga	agg cgc gcc ccc tgg	gag gat cct gcc	6850											
Gly Leu Gln Leu Tyr Gly	Arg Ala Pro Trp Glu	Asp Pro Ala												
2270	2275	2280												
aag tgg gtg atg gac aca	tat cca tgg gca gcc	agc cca caa cag	6895											
Lys Trp Val Met Asp Thr	Tyr Pro Trp Ala Ala Ser	Pro Gln Gln												
2285	2290	2295												
cac gag tgg cct ccc ctg	ctg cag tta cgg cct	gag gat gtc ggc	6940											
His Glu Trp Pro Pro Leu	Leu Gln Leu Arg Pro Glu	Asp Val Gly												
2300	2305	2310												
ttc gac ggc tac tcc atg	cct cgg gag gga tcg	aca agc aag cag	6985											
Phe Asp Gly Tyr Ser Met	Pro Arg Glu Gly Ser Thr	Ser Lys Gln												
2315	2320	2325												
atg ccc ccc agt gat gct	gaa ggt gac ccg ctg	atg aac atg ctg	7030											
Met Pro Pro Ser Asp Ala	Glu Gly Asp Pro Leu Met	Asn Met Leu												
2330	2335	2340												
atg agg ctg cag gag gca	gcc aac tac tcc agc	ccc cag agc tat	7075											
Met Arg Leu Gln Glu Ala	Ala Asn Tyr Ser Ser Pro	Gln Ser Tyr												
2345	2350	2355												
gac agc gac tcc aac agc	aac agc cat cac gat	gac atc ttg gac	7120											
Asp Ser Asp Ser Asn Ser	Asn Ser His His Asp Asp	Ile Leu Asp												
2360	2365	2370												
tcc tct ttg gag tcc act	ctg tgacaggggc ccggagccca	gcgccctcct	7171											
Ser Ser Leu Glu Ser Thr	Leu													
2375	2380													
ctttctctca ccgcattcca cctgcatccc ccacatcacc ctgaagatga cttcctgagc			7231											
cagccccag ccacagcctt agagctgcgg gaacaccgag acccccgcgc cttcagcctc			7291											
gacctgggtg caggcatccc gggccagctg cctgcggacc gcttccttcc acagcgagaa			7351											
ctgcactacc ttctgttgta ctttaattat tgttttgcct tgttgctgtg acctccctaa			7411											
gacactgaag atacttctcg ggaaaggatc atcgccgttg aaatgaaaag agagacagag			7471											
agagaaaaaa aaaagagaac ccacatgaag ctctgaaacc aaacagcatc ctgccatgag			7531											
cttcccagag acagaagaga ctggagcaaa gtcggaaaca cagagaagca cggcttcccc			7591											
tcagcacaga ccctccagac tgggtctcag agccgtgccca cccaccctcc cacacagccg			7651											

Corrected Sequence Listing2.ST25

gccacagggga gaactggtgc taaccagggt gcttgctttg gtcacgttca acgcactaca 7711
gagctacgac acaggggaac cttaggagca aataaaccgt gctttcatgt tttttaaaaa 7771
aaaaaaaaaa aa 7783

<210> 27
<211> 2380
<212> PRT
<213> Homo sapiens

<400> 27

Asn Gln Pro Glu Arg Leu Asn Ser Gln Val Leu Gln Gly Leu Gln Glu
1 5 10 15

Pro Ala Gly Glu Gly Leu Pro Leu Arg Lys Ser Gly Ser Val Glu Asn
20 25 30

Gly Phe Asp Thr Gln Ile Tyr Thr Asp Trp Ala Asn His Tyr Leu Ala
35 40 45

Lys Ser Gly His Lys Arg Leu Ile Arg Asp Leu Gln Gln Asp Val Thr
50 55 60

Asp Gly Val Leu Leu Ala Gln Ile Ile Gln Val Val Ala Asn Glu Lys
65 70 75 80

Ile Glu Asp Ile Asn Gly Cys Pro Lys Asn Arg Ser Gln Met Ile Glu
85 90 95

Asn Ile Asp Ala Cys Leu Asn Phe Leu Ala Ala Lys Gly Ile Asn Ile
100 105 110

Gln Gly Leu Ser Ala Glu Glu Ile Arg Asn Gly Asn Leu Lys Ala Ile
115 120 125

Leu Gly Leu Phe Phe Ser Leu Ser Arg Tyr Lys Gln Gln Gln Gln Gln
130 135 140

Pro Gln Lys Gln His Leu Ser Ser Pro Leu Pro Pro Ala Val Ser Gln
145 150 155 160

Val Ala Gly Ala Pro Ser Gln Cys Gln Ala Gly Thr Pro Gln Gln Gln
165 170 175

Val Pro Val Thr Pro Gln Ala Pro Cys Gln Pro His Gln Pro Ala Pro
180 185 190

Corrected Sequence Listing2.ST25

His Gln Gln Ser Lys Ala Gln Ala Glu Met Gln Ser Arg Leu Pro Gly
195 200 205

Pro Thr Ala Arg Val Ser Ala Ala Gly Ser Glu Ala Lys Thr Arg Gly
210 215 220

Gly Ser Thr Thr Ala Asn Asn Arg Arg Ser Gln Ser Phe Asn Asn Tyr
225 230 235 240

Asp Lys Ser Lys Pro Val Thr Ser Pro Pro Pro Pro Ser Ser His
245 250 255

Glu Lys Glu Pro Leu Ala Ser Ser Ala Ser Ser His Pro Gly Met Ser
260 265 270

Asp Asn Ala Pro Ala Ser Leu Glu Ser Gly Ser Ser Ser Thr Pro Thr
275 280 285

Asn Cys Ser Thr Ser Ser Ala Ile Pro Gln Pro Gly Ala Ala Thr Lys
290 295 300

Pro Trp Arg Ser Lys Ser Leu Ser Val Lys His Ser Ala Thr Val Ser
305 310 315 320

Met Leu Ser Val Lys Pro Pro Gly Pro Glu Ala Pro Arg Pro Thr Pro
325 330 335

Glu Ala Met Lys Pro Ala Pro Asn Asn Gln Lys Ser Met Leu Glu Lys
340 345 350

Leu Lys Leu Phe Asn Ser Lys Gly Gly Ser Lys Ala Gly Glu Gly Pro
355 360 365

Gly Ser Arg Asp Thr Ser Cys Glu Arg Leu Glu Thr Leu Pro Ser Phe
370 375 380

Glu Glu Ser Glu Glu Leu Glu Ala Ala Ser Arg Met Leu Thr Thr Val
385 390 395 400

Gly Pro Ala Ser Ser Ser Pro Lys Ile Ala Leu Lys Gly Ile Ala Gln
405 410 415

Arg Thr Phe Ser Arg Ala Leu Thr Asn Lys Lys Ser Ser Leu Lys Gly
420 425 430

Asn Glu Lys Glu Lys Glu Lys Gln Gln Arg Glu Lys Asp Lys Glu Lys
435 440 445

Corrected Sequence Listing2.ST25

Ser Lys Asp Leu Ala Lys Arg Ala Ser Val Thr Glu Arg Leu Asp Leu
450 455 460

Lys Glu Glu Pro Lys Glu Asp Pro Ser Gly Ala Ala Val Pro Glu Met
465 470 475 480

Pro Lys Lys Ser Ser Lys Ile Ala Ser Phe Ile Pro Lys Gly Gly Lys
485 490 495

Leu Asn Ser Ala Lys Lys Glu Pro Met Ala Pro Ser His Ser Gly Ile
500 505 510

Pro Lys Pro Gly Met Lys Ser Met Pro Gly Lys Ser Pro Ser Ala Pro
515 520 525

Ala Pro Ser Lys Glu Gly Glu Arg Ser Arg Ser Gly Lys Leu Ser Ser
530 535 540

Gly Leu Pro Gln Gln Lys Pro Gln Leu Asp Gly Arg His Ser Ser Ser
545 550 555 560

Ser Ser Ser Leu Ala Ser Ser Glu Gly Lys Gly Pro Gly Gly Thr Thr
565 570 575

Leu Asn His Ser Ile Ser Ser Gln Thr Val Ser Gly Ser Val Gly Thr
580 585 590

Thr Gln Thr Thr Gly Ser Asn Thr Val Ser Val Gln Leu Pro Gln Pro
595 600 605

Gln Gln Gln Tyr Asn His Pro Asn Thr Ala Thr Val Ala Pro Phe Leu
610 615 620

Tyr Arg Ser Gln Thr Asp Thr Glu Gly Asn Val Thr Ala Glu Ser Ser
625 630 635 640

Ser Thr Gly Val Ser Val Glu Pro Ser His Phe Thr Lys Thr Gly Gln
645 650 655

Pro Ala Leu Glu Glu Leu Thr Gly Glu Asp Pro Glu Ala Arg Arg Leu
660 665 670

Arg Thr Val Lys Asn Ile Ala Asp Leu Arg Gln Asn Leu Glu Glu Thr
675 680 685

Met Ser Ser Leu Arg Gly Thr Gln Val Thr His Ser Thr Leu Glu Thr
690 695 700

Corrected Sequence Listing2.ST25

Thr Phe Asp Thr Asn Val Thr Thr Glu Met Ser Gly Arg Ser Ile Leu
705 710 715 720

Ser Leu Thr Gly Arg Pro Thr Pro Leu Ser Trp Arg Leu Gly Gln Ser
725 730 735

Ser Pro Arg Leu Gln Ala Gly Asp Ala Pro Ser Met Gly Asn Gly Tyr
740 745 750

Pro Pro Arg Ala Asn Ala Ser Arg Phe Ile Asn Thr Glu Ser Gly Arg
755 760 765

Tyr Val Tyr Ser Ala Pro Leu Arg Arg Gln Leu Ala Ser Arg Gly Ser
770 775 780

Ser Val Cys His Val Asp Val Ser Asp Lys Ala Gly Asp Glu Met Asp
785 790 795 800

Leu Glu Gly Ile Ser Met Asp Ala Pro Gly Tyr Met Ser Asp Gly Asp
805 810 815

Val Leu Ser Lys Asn Ile Arg Thr Asp Asp Ile Thr Ser Gly Tyr Met
820 825 830

Thr Asp Gly Gly Leu Gly Leu Tyr Thr Arg Arg Leu Asn Arg Leu Pro
835 840 845

Asp Gly Met Ala Val Val Arg Glu Thr Leu Gln Arg Asn Thr Ser Leu
850 855 860

Gly Leu Gly Asp Ala Asp Ser Trp Asp Asp Ser Ser Ser Val Ser Ser
865 870 875 880

Gly Ile Ser Asp Thr Ile Asp Asn Leu Ser Thr Asp Asp Ile Asn Thr
885 890 895

Ser Ser Ser Ile Ser Ser Tyr Ala Asn Thr Pro Ala Ser Ser Arg Lys
900 905 910

Asn Leu Asp Val Gln Thr Asp Ala Glu Lys His Ser Gln Val Glu Arg
915 920 925

Asn Ser Leu Trp Ser Gly Asp Asp Val Lys Lys Ser Asp Gly Gly Ser
930 935 940

Asp Ser Gly Ile Lys Met Glu Pro Gly Ser Lys Trp Arg Arg Asn Pro
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Corrected Sequence Listing2.ST25

945	Corrected Sequence Listing213125										955	960									
Ser	Asp	Val	Ser	Asp	Glu	Ser	Asp	Lys	Ser	Thr	Ser	Gly	Lys	Lys	Asn						
			965						970					975							
Pro	Val	Ile	Ser	Gln	Thr	Gly	Ser	Trp	Arg	Arg	Gly	Met	Thr	Ala	Gln						
			980					985					990								
Val	Gly	Ile	Thr	Met	Pro	Arg	Thr	Lys	Ala	Ser	Ala	Pro	Ala	Gly	Ala						
		995					1000					1005									
Leu	Lys	Thr	Pro	Gly	Thr	Gly	Lys	Thr	Asp	Asp	Ala	Lys	Val	Ser							
	1010					1015					1020										
Glu	Lys	Gly	Arg	Leu	Ser	Pro	Lys	Ala	Ser	Gln	Val	Lys	Arg	Ser							
	1025					1030					1035										
Pro	Ser	Asp	Ala	Gly	Arg	Ser	Ser	Gly	Asp	Glu	Ser	Lys	Lys	Pro							
	1040					1045					1050										
Leu	Pro	Ser	Ser	Ser	Arg	Thr	Pro	Thr	Ala	Asn	Ala	Asn	Ser	Phe							
	1055					1060					1065										
Gly	Phe	Lys	Lys	Gln	Ser	Gly	Ser	Ala	Thr	Gly	Leu	Ala	Met	Ile							
	1070					1075					1080										
Thr	Ala	Ser	Gly	Val	Thr	Val	Thr	Ser	Arg	Ser	Ala	Thr	Leu	Gly							
	1085					1090					1095										
Lys	Ile	Pro	Lys	Ser	Ser	Ala	Leu	Val	Ser	Arg	Ser	Ala	Gly	Arg							
	1100					1105					1110										
Lys	Ser	Ser	Met	Asp	Gly	Ala	Gln	Asn	Gln	Asp	Asp	Gly	Tyr	Leu							
	1115					1120					1125										
Ala	Leu	Ser	Ser	Arg	Thr	Asn	Leu	Gln	Tyr	Arg	Ser	Leu	Pro	Arg							
	1130					1135					1140										
Pro	Ser	Lys	Ser	Asn	Ser	Arg	Asn	Gly	Ala	Gly	Asn	Arg	Ser	Ser							
	1145					1150					1155										
Thr	Ser	Ser	Ile	Asp	Ser	Asn	Ile	Ser	Ser	Lys	Ser	Ala	Gly	Leu							
	1160					1165					1170										
Pro	Val	Pro	Lys	Leu	Arg	Glu	Pro	Ser	Lys	Thr	Ala	Leu	Gly	Ser							
	1175					1180					1185										

Corrected Sequence Listing2.ST25

Ser	Leu	Pro	Gly	Leu	Val	Asn	Gln	Thr	Asp	Lys	Glu	Lys	Gly	Ile
1190						1195					1200			
Ser	Ser	Asp	Asn	Glu	Ser	Val	Ala	Ser	Cys	Asn	Ser	Val	Lys	Val
1205						1210					1215			
Asn	Pro	Ala	Ala	Gln	Pro	Val	Ser	Ser	Pro	Ala	Gln	Thr	Ser	Leu
1220						1225					1230			
Gln	Pro	Gly	Ala	Lys	Tyr	Pro	Asp	Val	Ala	Ser	Pro	Thr	Leu	Arg
1235						1240					1245			
Arg	Leu	Phe	Gly	Gly	Lys	Pro	Thr	Lys	Gln	Val	Pro	Ile	Ala	Thr
1250						1255					1260			
Ala	Glu	Asn	Met	Lys	Asn	Ser	Val	Val	Ile	Ser	Asn	Pro	His	Ala
1265						1270					1275			
Thr	Met	Thr	Gln	Gln	Gly	Asn	Leu	Asp	Ser	Pro	Ser	Gly	Ser	Gly
1280						1285					1290			
Val	Leu	Ser	Ser	Gly	Ser	Ser	Pro	Leu	Tyr	Ser	Lys	Asn	Val	
1295						1300				1305				
Asp	Leu	Asn	Gln	Ser	Pro	Leu	Ala	Ser	Ser	Pro	Ser	Ser	Ala	His
1310						1315					1320			
Ser	Ala	Pro	Ser	Asn	Ser	Leu	Thr	Trp	Gly	Thr	Asn	Ala	Ser	Ser
1325						1330					1335			
Ser	Ser	Ala	Val	Ser	Lys	Asp	Gly	Leu	Gly	Phe	Gln	Ser	Val	Ser
1340						1345					1350			
Ser	Leu	His	Thr	Ser	Cys	Glu	Ser	Ile	Asp	Ile	Ser	Leu	Ser	Ser
1355						1360					1365			
Gly	Gly	Val	Pro	Ser	His	Asn	Ser	Ser	Thr	Gly	Leu	Ile	Ala	Ser
1370						1375					1380			
Ser	Lys	Asp	Asp	Ser	Leu	Thr	Pro	Phe	Val	Arg	Thr	Asn	Ser	Val
1385						1390					1395			
Lys	Thr	Thr	Leu	Ser	Glu	Ser	Pro	Leu	Ser	Ser	Pro	Ala	Ala	Ser
1400						1405					1410			
Pro	Lys	Phe	Cys	Arg	Ser	Thr	Leu	Pro	Arg	Lys	Gln	Asp	Ser	Asp
1415						1420					1425			

Corrected Sequence Listing2.ST25

Pro	His	Leu	Asp	Arg	Asn	Thr	Leu	Pro	Lys	Lys	Gly	Leu	Arg	Tyr
	1430					1435					1440			
Thr	Pro	Thr	Ser	Gln	Leu	Arg	Thr	Gln	Glu	Asp	Ala	Lys	Glu	Trp
	1445					1450					1455			
Leu	Arg	Ser	His	Ser	Ala	Gly	Gly	Leu	Gln	Asp	Thr	Ala	Ala	Asn
	1460					1465					1470			
Ser	Pro	Phe	Ser	Ser	Gly	Ser	Ser	Val	Thr	Ser	Pro	Ser	Gly	Thr
	1475					1480					1485			
Arg	Phe	Asn	Phe	Ser	Gln	Leu	Ala	Ser	Pro	Thr	Thr	Val	Thr	Gln
	1490					1495					1500			
Met	Ser	Leu	Ser	Asn	Pro	Thr	Met	Leu	Arg	Thr	His	Ser	Leu	Ser
	1505					1510					1515			
Asn	Ala	Asp	Gly	Gln	Tyr	Asp	Pro	Tyr	Thr	Asp	Ser	Arg	Phe	Arg
	1520					1525					1530			
Asn	Ser	Ser	Met	Ser	Leu	Asp	Glu	Lys	Ser	Arg	Thr	Met	Ser	Arg
	1535					1540					1545			
Ser	Gly	Ser	Phe	Arg	Asp	Gly	Phe	Glu	Glu	Val	His	Gly	Ser	Ser
	1550					1555					1560			
Leu	Ser	Leu	Val	Ser	Ser	Thr	Ser	Ser	Val	Tyr	Ser	Thr	Pro	Glu
	1565					1570					1575			
Glu	Lys	Cys	Gln	Ser	Glu	Ile	Arg	Lys	Leu	Arg	Arg	Glu	Leu	Asp
	1580					1585					1590			
Ala	Ser	Gln	Glu	Lys	Val	Ser	Ala	Leu	Thr	Thr	Gln	Leu	Thr	Ala
	1595					1600					1605			
Asn	Ala	His	Leu	Val	Ala	Ala	Phe	Glu	Gln	Ser	Leu	Gly	Asn	Met
	1610					1615					1620			
Thr	Ile	Arg	Leu	Gln	Ser	Leu	Thr	Met	Thr	Ala	Glu	Gln	Lys	Asp
	1625					1630					1635			
Ser	Glu	Leu	Asn	Glu	Leu	Arg	Lys	Thr	Ile	Glu	Leu	Leu	Lys	Lys
	1640					1645					1650			
Gln	Asn	Ala	Ala	Ala	Gln	Ala	Ala	Ile	Asn	Gly	Val	Ile	Asn	Thr
	1655					1660					1665			

Corrected Sequence Listing2.ST25

Pro	Glu	Leu	Asn	Cys	Lys	Gly	Asn	Gly	Thr	Ala	Gln	Ser	Ala	Asp
	1670					1675					1680			
Leu	Arg	Ile	Arg	Arg	Gln	His	Ser	Ser	Asp	Ser	Val	Ser	Ser	Ile
	1685					1690					1695			
Asn	Ser	Ala	Thr	Ser	His	Ser	Ser	Val	Gly	Ser	Asn	Ile	Glu	Ser
	1700					1705					1710			
Asp	Ser	Lys	Lys	Lys	Lys	Arg	Lys	Asn	Trp	Val	Asn	Glu	Leu	Arg
	1715					1720					1725			
Ser	Ser	Phe	Lys	Gln	Ala	Phe	Gly	Lys	Lys	Lys	Ser	Pro	Lys	Ser
	1730					1735					1740			
Ala	Ser	Ser	His	Ser	Asp	Ile	Glu	Glu	Met	Thr	Asp	Ser	Ser	Leu
	1745					1750					1755			
Pro	Ser	Ser	Pro	Lys	Leu	Pro	His	Asn	Gly	Ser	Thr	Gly	Ser	Thr
	1760					1765					1770			
Pro	Leu	Leu	Arg	Asn	Ser	His	Ser	Asn	Ser	Leu	Ile	Ser	Glu	Cys
	1775					1780					1785			
Met	Asp	Ser	Glu	Ala	Glu	Thr	Val	Met	Gln	Leu	Arg	Asn	Glu	Leu
	1790					1795					1800			
Arg	Asp	Lys	Glu	Met	Lys	Leu	Thr	Asp	Ile	Arg	Leu	Glu	Ala	Leu
	1805					1810					1815			
Ser	Ser	Ala	His	Gln	Leu	Asp	Gln	Leu	Arg	Glu	Ala	Met	Asn	Arg
	1820					1825					1830			
Met	Gln	Ser	Glu	Ile	Glu	Lys	Leu	Lys	Ala	Glu	Asn	Asp	Arg	Leu
	1835					1840					1845			
Lys	Ser	Glu	Ser	Gln	Gly	Ser	Gly	Cys	Ser	Arg	Ala	Pro	Ser	Gln
	1850					1855					1860			
Val	Ser	Ile	Ser	Ala	Ser	Pro	Arg	Gln	Ser	Met	Gly	Leu	Ser	Gln
	1865					1870					1875			
His	Ser	Leu	Asn	Leu	Thr	Glu	Ser	Thr	Ser	Leu	Asp	Met	Leu	Leu
	1880					1885					1890			
Asp	Asp	Thr	Gly	Glu	Cys	Ser	Ala	Arg	Lys	Glu	Gly	Gly	Arg	His

Corrected Sequence Listing2.ST25
1900 1905

1895
Val Lys Ile Val Val Ser Phe Gln Glu Glu Met Lys Trp Lys Glu
1910 1915 1920
Asp Ser Arg Pro His Leu Phe Leu Ile Gly Cys Ile Gly Val Ser
1925 1930 1935
Gly Lys Thr Lys Trp Asp Val Leu Asp Gly Val Val Arg Arg Leu
1940 1945 1950
Phe Lys Glu Tyr Ile Ile His Val Asp Pro Val Ser Gln Leu Gly
1955 1960 1965
Leu Asn Ser Asp Ser Val Leu Gly Tyr Ser Ile Gly Glu Ile Lys
1970 1975 1980
Arg Ser Asn Thr Ser Glu Thr Pro Glu Leu Leu Pro Cys Gly Tyr
1985 1990 1995
Leu Val Gly Glu Asn Thr Thr Ile Ser Val Thr Val Lys Gly Leu
2000 2005 2010
Ala Glu Asn Ser Leu Asp Ser Leu Val Phe Glu Ser Leu Ile Pro
2015 2020 2025
Lys Pro Ile Leu Gln Arg Tyr Val Ser Leu Leu Ile Glu His Arg
2030 2035 2040
Arg Ile Ile Leu Ser Gly Pro Ser Gly Thr Gly Lys Thr Tyr Leu
2045 2050 2055
Ala Asn Arg Leu Ser Glu Tyr Ile Val Leu Arg Glu Gly Arg Glu
2060 2065 2070
Leu Thr Asp Gly Val Ile Ala Thr Phe Asn Val Asp His Lys Ser
2075 2080 2085
Ser Lys Glu Leu Arg Gln Tyr Leu Ser Asn Leu Ala Asp Gln Cys
2090 2095 2100
Asn Ser Glu Asn Asn Ala Val Asp Met Pro Leu Val Ile Ile Leu
2105 2110 2115
Asp Asn Leu His His Val Ser Ser Leu Gly Glu Ile Phe Asn Gly
2120 2125 2130

Corrected Sequence Listing2.ST25

Leu	Leu	Asn	Cys	Lys	Tyr	His	Lys	Cys	Pro	Tyr	Ile	Ile	Gly	Thr
	2135					2140					2145			
Met	Asn	Gln	Ala	Thr	Ser	Ser	Thr	Pro	Asn	Leu	Gln	Leu	His	His
	2150					2155					2160			
Asn	Phe	Arg	Trp	Val	Leu	Cys	Ala	Asn	His	Thr	Glu	Pro	Val	Lys
	2165					2170					2175			
Gly	Phe	Leu	Gly	Arg	Phe	Leu	Arg	Arg	Lys	Leu	Met	Glu	Thr	Glu
	2180					2185					2190			
Ile	Ser	Gly	Arg	Val	Arg	Asn	Met	Glu	Leu	Val	Lys	Ile	Ile	Asp
	2195					2200					2205			
Trp	Ile	Pro	Lys	Val	Trp	His	His	Leu	Asn	Arg	Phe	Leu	Glu	Ala
	2210					2215					2220			
His	Ser	Ser	Ser	Asp	Val	Thr	Ile	Gly	Pro	Arg	Leu	Phe	Leu	Ser
	2225					2230					2235			
Cys	Pro	Ile	Asp	Val	Asp	Gly	Ser	Arg	Val	Trp	Phe	Thr	Asp	Leu
	2240					2245					2250			
Trp	Asn	Tyr	Ser	Ile	Ile	Pro	Tyr	Leu	Leu	Glu	Ala	Val	Arg	Glu
	2255					2260					2265			
Gly	Leu	Gln	Leu	Tyr	Gly	Arg	Arg	Ala	Pro	Trp	Glu	Asp	Pro	Ala
	2270					2275					2280			
Lys	Trp	Val	Met	Asp	Thr	Tyr	Pro	Trp	Ala	Ala	Ser	Pro	Gln	Gln
	2285					2290					2295			
His	Glu	Trp	Pro	Pro	Leu	Leu	Gln	Leu	Arg	Pro	Glu	Asp	Val	Gly
	2300					2305					2310			
Phe	Asp	Gly	Tyr	Ser	Met	Pro	Arg	Glu	Gly	Ser	Thr	Ser	Lys	Gln
	2315					2320					2325			
Met	Pro	Pro	Ser	Asp	Ala	Glu	Gly	Asp	Pro	Leu	Met	Asn	Met	Leu
	2330					2335					2340			
Met	Arg	Leu	Gln	Glu	Ala	Ala	Asn	Tyr	Ser	Ser	Pro	Gln	Ser	Tyr
	2345					2350					2355			
Asp	Ser	Asp	Ser	Asn	Ser	Asn	Ser	His	His	Asp	Asp	Ile	Leu	Asp
	2360					2365					2370			

Corrected Sequence Listing2.ST25

Ser Ser Leu Glu Ser Thr Leu
2375 2380

<210> 28
<211> 96
<212> DNA
<213> Homo sapiens

<220>
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<223>

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Ser Arg Glu Arg Gly Gly Ser Val Pro Ser Leu Leu Gln Gly Gln Cys
1 5 10 15
ccc agc ctc agc cac act tct gat ctg cag tcc aac aga cct ttc tag 96
Pro Ser Leu Ser His Thr Ser Asp Leu Gln Ser Asn Arg Pro Phe
20 25 30

<210> 29
<211> 75
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(72)
<223>

<400> 29
cat gcc aaa gag aac ctg ggg gtg cca ggg ggt cct cag agc tca cac 48
His Ala Lys Glu Asn Leu Gly Val Pro Gly Gly Pro Gln Ser Ser His
1 5 10 15
tgc act tgt ggc acc cac agc gag tag 75
Cys Thr Cys Gly Thr His Ser Glu
20

<210> 30
<211> 489
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(489)
<223>

<400> 30
cca tcc gtg agc cga gga aac tgt aca cag atc tac aca gac tgg gcc 48
Pro Ser Val Ser Arg Gly Asn Cys Thr Gln Ile Tyr Thr Asp Trp Ala
1 5 10 15
aat cat tac cta gcc aaa tcc ggc cac aag cgt ctc atc aag gat ctc 96
Asn His Tyr Leu Ala Lys Ser Gly His Lys Arg Leu Ile Lys Asp Leu
20 25 30

Corrected Sequence Listing2.ST25

cag caa gat gtg aca gat ggc gtc ctc ctg gcc cag att atc cag gtt Gln Gln Asp Val Thr Asp Gly Val Leu Leu Ala Gln Ile Ile Gln Val 35 40 45	144
gtg gca aat gaa aag att gaa gac atc aat ggc tgt ccg aag aac aga Val Ala Asn Glu Lys Ile Glu Asp Ile Asn Gly Cys Pro Lys Asn Arg 50 55 60	192
tcc caa atg att gaa aac ata gat gcc tgc ttg aat ttc ctg gca gct Ser Gln Met Ile Glu Asn Ile Asp Ala Cys Leu Asn Phe Leu Ala Ala 65 70 75 80	240
aag gga ata aac atc cag ggg ctg tct gca gaa gag atc agg aat gga Lys Gly Ile Asn Ile Gln Gly Leu Ser Ala Glu Glu Ile Arg Asn Gly 85 90 95	288
aac ctc aag gcc att cta ggc ctc ttc ttc agc ctc tcc cga tac aag Asn Leu Lys Ala Ile Leu Gly Leu Phe Phe Ser Leu Ser Arg Tyr Lys 100 105 110	336
cag cag cag cag cag ccc cag aag cag cac ctc tcc tca cct ctg ccg Gln Gln Gln Gln Gln Pro Gln Lys Gln His Leu Ser Ser Pro Leu Pro 115 120 125	384
ccc gcc gta tcc cag gtg gcc ggg gcc ccc tcc cag tgc cag gct ggc Pro Ala Val Ser Gln Val Ala Gly Ala Pro Ser Gln Cys Gln Ala Gly 130 135 140	432
acc cct cag cag cag gtg cca gtc act ccc caa gcc ccg tgc cag cct Thr Pro Gln Gln Gln Val Pro Val Thr Pro Gln Ala Pro Cys Gln Pro 145 150 155 160	480
cac cag cca His Gln Pro	489

<210> 31
 <211> 31
 <212> PRT
 <213> Homo sapiens

<400> 31

Ser Arg Glu Arg Gly Gly Ser Val Pro Ser Leu Leu Gln Gly Gln Cys
 1 5 10 15

Pro Ser Leu Ser His Thr Ser Asp Leu Gln Ser Asn Arg Pro Phe
 20 25 30

<210> 32
 <211> 24
 <212> PRT
 <213> Homo sapiens

<400> 32

His Ala Lys Glu Asn Leu Gly Val Pro Gly Gly Pro Gln Ser Ser His
 1 5 10 15

Corrected Sequence Listing2.ST25

Cys Thr Cys Gly Thr His Ser Glu
20

<210> 33
<211> 163
<212> PRT
<213> Homo sapiens

<400> 33

Pro Ser Val Ser Arg Gly Asn Cys Thr Gln Ile Tyr Thr Asp Trp Ala
1 5 10 15

Asn His Tyr Leu Ala Lys Ser Gly His Lys Arg Leu Ile Lys Asp Leu
20 25 30

Gln Gln Asp Val Thr Asp Gly Val Leu Leu Ala Gln Ile Ile Gln Val
35 40 45

Val Ala Asn Glu Lys Ile Glu Asp Ile Asn Gly Cys Pro Lys Asn Arg
50 55 60

Ser Gln Met Ile Glu Asn Ile Asp Ala Cys Leu Asn Phe Leu Ala Ala
65 70 75 80

Lys Gly Ile Asn Ile Gln Gly Leu Ser Ala Glu Glu Ile Arg Asn Gly
85 90 95

Asn Leu Lys Ala Ile Leu Gly Leu Phe Phe Ser Leu Ser Arg Tyr Lys
100 105 110

Gln Gln Gln Gln Gln Pro Gln Lys Gln His Leu Ser Ser Pro Leu Pro
115 120 125

Pro Ala Val Ser Gln Val Ala Gly Ala Pro Ser Gln Cys Gln Ala Gly
130 135 140

Thr Pro Gln Gln Gln Val Pro Val Thr Pro Gln Ala Pro Cys Gln Pro
145 150 155 160

His Gln Pro

<210> 34
<211> 479
<212> DNA
<213> Mouse

<220>
<221> CDS

Corrected Sequence Listing2.ST25

<222> (3)..(476)

<223>

<400> 34

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	Glu	Lys	Ser	Arg	Thr	Met	Ser	Arg	Ser	Gly	Ser	Phe	Arg	Asp	Gly	
1					5					10					15	

ttt	gag	gaa	gtt	cat	gga	tcc	tcc	ctg	tcc	ttg	gtt	tcc	agc	aca	tcc	95
Phe	Glu	Glu	Val	His	Gly	Ser	Ser	Leu	Ser	Leu	Val	Ser	Ser	Thr	Ser	
				20					25					30		

tcc	atc	tac	tcc	acg	cca	gaa	gaa	aaa	tgc	cag	tca	gag	att	cga	aag	143
Ser	Ile	Tyr	Ser	Thr	Pro	Glu	Glu	Lys	Cys	Gln	Ser	Glu	Ile	Arg	Lys	
			35					40					45			

ctg	agg	cga	gaa	ctg	gat	gcc	tcc	cag	gaa	aag	gtg	tct	gcg	ctg	act	191
Leu	Arg	Arg	Glu	Leu	Asp	Ala	Ser	Gln	Glu	Lys	Val	Ser	Ala	Leu	Thr	
		50				55						60				

acc	cag	ctg	act	gca	aat	gct	cac	ctt	gtg	gca	gcc	ttc	gag	cag	agt	239
Thr	Gln	Leu	Thr	Ala	Asn	Ala	His	Leu	Val	Ala	Ala	Phe	Glu	Gln	Ser	
	65					70					75					

ctg	gga	aac	atg	acc	atc	agg	cta	cag	agt	tta	act	atg	acc	gct	gag	287
Leu	Gly	Asn	Met	Thr	Ile	Arg	Leu	Gln	Ser	Leu	Thr	Met	Thr	Ala	Glu	
80					85					90					95	

cag	aag	gat	tca	gaa	ctg	aac	gag	tta	aga	aaa	acc	atc	gag	ctg	ctg	335
Gln	Lys	Asp	Ser	Glu	Leu	Asn	Glu	Leu	Arg	Lys	Thr	Ile	Glu	Leu	Leu	
				100					105					110		

aag	aaa	cag	aat	gca	gct	gcc	cag	gct	gcc	att	aat	gga	gtg	att	aac	383
Lys	Lys	Gln	Asn	Ala	Ala	Ala	Gln	Ala	Ala	Ile	Asn	Gly	Val	Ile	Asn	
			115					120					125			

acg	cca	gag	ctc	aac	tgc	aaa	gga	aat	ggc	agt	gcc	agg	cta	cag	acc	431
Thr	Pro	Glu	Leu	Asn	Cys	Lys	Gly	Asn	Gly	Ser	Ala	Arg	Leu	Gln	Thr	
		130					135					140				

tac	gca	tcc	gca	gca	aca	ctc	ctc	cga	cag	tgt	ctc	cag	tat	caa	tag	479
Tyr	Ala	Ser	Ala	Ala	Thr	Leu	Leu	Arg	Gln	Cys	Leu	Gln	Tyr	Gln		
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<210> 35

<211> 22

<212> DNA

<213> Mouse

<220>

<221> CDS

<222> (1)..(21)

<223>

<400> 35

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Arg	His	Gln	Pro	Leu	Lys	Cys		
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<210> 36

<211> 158

Corrected Sequence Listing2.ST25

<212> PRT

<213> Mouse

<400> 36

Glu Lys Ser Arg Thr Met Ser Arg Ser Gly Ser Phe Arg Asp Gly Phe
1 5 10 15

Glu Glu Val His Gly Ser Ser Leu Ser Leu Val Ser Ser Thr Ser Ser
20 25 30

Ile Tyr Ser Thr Pro Glu Glu Lys Cys Gln Ser Glu Ile Arg Lys Leu
35 40 45

Arg Arg Glu Leu Asp Ala Ser Gln Glu Lys Val Ser Ala Leu Thr Thr
50 55 60

Gln Leu Thr Ala Asn Ala His Leu Val Ala Ala Phe Glu Gln Ser Leu
65 70 75 80

Gly Asn Met Thr Ile Arg Leu Gln Ser Leu Thr Met Thr Ala Glu Gln
85 90 95

Lys Asp Ser Glu Leu Asn Glu Leu Arg Lys Thr Ile Glu Leu Leu Lys
100 105 110

Lys Gln Asn Ala Ala Ala Gln Ala Ala Ile Asn Gly Val Ile Asn Thr
115 120 125

Pro Glu Leu Asn Cys Lys Gly Asn Gly Ser Ala Arg Leu Gln Thr Tyr
130 135 140

Ala Ser Ala Ala Thr Leu Leu Arg Gln Cys Leu Gln Tyr Gln
145 150 155

<210> 37

<211> 7

<212> PRT

<213> Mouse

<400> 37

Arg His Gln Pro Leu Lys Cys
1 5

<210> 38

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide for production of AK

Corrected Sequence Listing2.ST25

<400> 38

Glu Lys Gly Glu Asp Pro Glu Thr Arg Arg Met Arg Thr Val Lys Asn
1 5 10 15

Ile Ala Asp

<210> 39
<211> 81369
<212> DNA
<213> Homo sapiens

<220>
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<222> (109)..(109)
<223> n = a, g, t, or c

<220>
<221> misc_feature
<222> (6825)..(6825)
<223> n = a, g, t, or c

<220>
<221> misc_feature
<222> (6842)..(6842)
<223> n = a, g, t, or c

<220>
<221> misc_feature
<222> (6863)..(6863)
<223> n = a, g, t, or c

<220>
<221> misc_feature
<222> (80984)..(80984)
<223> n = a, g, t, or c

<220>
<221> misc_feature
<222> (81012)..(81012)
<223> n = a, g, t, or c

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tgagggtgca ttgcaaatcc aggctagagg gagagatacc agttaggana gtacagcaat 120
actctactgg gaaatggtga ggtgtttcgt gaagacaatg gcaacacaga tgaagacatg 180
cagatggagg aaataaagat ccagttgagc ttgttgacca gttggataga ggttgaggtt 240
atgcatgatg gagcaatcta gggttttgtc ttgggtaggt gtttccatga tagtactcag 300

Corrected Sequence Listing2.ST25

aatgaatcat atagttgtac aggttgaatc ccacccatgt ttgcacaata gagtgactgt	360
ctagctgaaa tccagatgac actctgtatg ctaagctatg cttcatggaa ctgtataaag	420
gcacttgcta cataggctag tggcagatct ggaagtaacc tatatgggtat ataggaaaatg	480
aggtggcttt tgtataaatc ctacagataa atttcatttc ctgacccat tattttgact	540
catgttagcc caagaagagt attcagtact tcatatccct gaaggtaaga cagagtagta	600
ttagattcac tatttggtcaa ataaaagggg tcaagtccta agatcaagct gatgaatcaa	660
cacctcatag gatatgtccc aaccaattat atggcttccc ctataaataa aatctagttc	720
tcttctctgg agaggaacag tgaagaatat cataacctat gctacaaact gcttgagtag	780
gagctacttc tctccaaggc tttatatcat tcattctggc agggccctct gtttgttctc	840
accagctcct gggaaattta tttctcctct agtgatataa aagctctctg tttgagatga	900
agggctgccc agtttatcag atctgtatta gtctgttctc aggctgctaa taaagacata	960
cctgagactg agtaatttat gaaggaaaga ggtttaattg actcacagtt ccacatggct	1020
ggggaggcct cacaatcatg gcgaaagact aataaggagc aaagtcacat cttacatggc	1080
tgcagacaag agagcatgtg caggggaact gctctccata aaaccatcag atcttgtag	1140
acttgttcac tattacaaga acaacagaca ggaaaacccg cccctcaat tcaattacct	1200
gccactggga ccctcccaca acacatgggg attatgagag ctacaattca agatgagatt	1260
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gaaacagaga ccagggtgtg ggaagtaagg tagtagcctg agagcagctg gcagtgtttt	1620
agacctggag ggaggttagg tcatcagcaa tgaggagact gcctggaaaa tcctagaaaa	1680
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cctttcctct gttaagagga ttcaagtgtc tttcttgcat tttgtcttct cttctatatc	1800
catgcttgca atataaggag acagcagttg gctgtttgtg ctagaaaata taaatggcca	1860
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tgttcttcag tgctgggatg tgaatctctt ggcaaacatc tctctaattc tgaactatct	1980
ttcaccacca tctagagata ttcacttact gaagtgcctt tttaaagcaa tgttcctcac	2040
caaggcgatg ttctgaatgt tttaaaatgg aagaatctgg aatgttttta ttataataca	2100
ttttgtatat cccaaagcaa aaatcaattt cttcatgggt aatacttttg taattttgtt	2160
tttaataata ttttcctttt aaatataaga aatattttat tgaattaata ctttaatgta	2220

Corrected Sequence Listing2.ST25

gctgtttcaa gtaagataaa acagaacaga ttactgtttt caaccttggt cacagttagc	2280
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ttcacttaac cttgaaatta tagtaatttg ggaacttcta ttcctctgaa agagaaagct	2400
aatgccaaag atattttcaag ggagaaagaa ggttttttaa aggagagaca attcagctca	2460
gacttaatag ctgtgattgc tatttattaa gcagaacgcc tataactaaa ttctcagata	2520
tccaaaaaac agcctgtaca ttctcaaaag tgaagattac acattttcta agttaaggta	2580
aaagttttgt ctctgtagca tcttactgat ttctatcttc tcattctgcc ttaataatgt	2640
cactaaataa atgtttgatg cactaataca tgaataaaac tattcatggg aatgattctt	2700
tagaaacaca gctaagtttt gtaattttgt tttttaaaaa ttaaaaattt aaatataaaa	2760
atgtttttta aaggcttgaa tttcttgta aatgtacaca ttttaagttg taggctgtct	2820
ttaaaaataa tctctccaca cactgtagta tttaaaacat catgatatta ctataaaaca	2880
tcaacaaata gggcagtggg aaacatggta atcactaaaa atgctcacat gtcatatatt	2940
aagacttgat aagtaaacca caataataaa tagaaaagaa atagttgtct aaaaagggat	3000
tctcaccttt caaaccttac cataaaaaatg gaatataaaa gaaggaagag gaggagaaat	3060
caaattatat cataaaattt tctgggcaaa aatattacag aagaaaataa gaaagattta	3120
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aacaaagaaa cagatttggg aaatatttga aactggtttt tttttagcat ttaaaaatgt	3240
aatacaaatg gattatttaa actccattgc aaaaatacac aaaggacatt gacaatgtct	3300
ggaaaataaa ttagctaagt aagttataga aaactcagt ctcacaattt gacaaatgta	3360
actgaaaact attaataata ttagtaacta tttttacatg tcaaaatttt tgaattacta	3420
aaggaaacca caatgcctga aagtatccag ggtttttttt tttttttata atattggcac	3480
tgtcatatgg gtggcaggaa ttgaagtgat gttgtttctt cagttattaa gttgcatctg	3540
cagtgtttca aatgtccaaa acctgtgagt cagtaattct ctttttgtat atttatccta	3600
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cttacaatag ttagaaaatt gtaaaatgct ttatgcatct taaaatataa attgttgaat	3720
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ttaagagcat taaaataatt ataaggtaat atgaagtga tgaataatgt acagatacta	3840
taatcagcag agtggttaact aggtaaattt ttatgtgtgt atatactact tcctaaaaat	3900
gacttgacag aaatcatcaa aatgctaatt gtggttactt ctgggtggga atacagatga	3960
tttactttgt tccttttatg tatttctgca ctgcccagtc ttccacagtg agcatatatt	4020
ggttttttaa tttatataag atggaaaaag ataccaaatg gtcttcaatg aatcctggag	4080

Corrected Sequence Listing2.ST25

ttaactttca	tgtgtgtcat	atgttatatt	ctaaacttat	cacaaataga	agacttttaa	4140
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acaaaaacca	accatcatga	ggattattca	agtaatgtgt	ttaaacaaaa	gaatttgtaa	4260
taaaattact	ttatctcctt	tgtgatttca	gccattttta	aaaaaataga	tgtttctact	4320
ctccttcaga	tatcattaaa	acataaaactt	gtgcctgact	gcataaatcc	cttttaaact	4380
aatatcactt	attacgttta	actaagtcta	cctagggctt	ccttgataaa	agaacaagag	4440
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cattatttat	attctagaga	aaataaaaagc	aaataaaaag	gtcagtgtat	aaagtttatt	4560
ggttgttctc	tttactcaaa	acccacatgg	tattaatggt	agtctctatg	aatatttcat	4620
ggataaaatc	agagcattaa	gtgcatacta	aaaacaataa	gaatggaaag	actttaacct	4680
tatgtttata	tgaatttcta	ggttatcaag	aagtttatag	gctataggct	ataaagtctt	4740
aggctatgat	atagtaacct	aatgtagact	tcccttgata	catgaaaata	atggtactaa	4800
gtacaaacag	aagatgagct	taaaattatt	ctttgagtcc	tcttgatgga	ttttttcccc	4860
cacactttcc	ccaaaattgt	tttatgccta	tattgtagga	gaccatgcaa	gagacctaga	4920
gtctcttttt	ctttcatcac	tttccaatca	acagcaaata	ctatcatttt	taccacaaaa	4980
tatatcttga	aactcccttc	ttttgattta	cttgtaactc	cccatcaaaa	actgaagagt	5040
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aaataccctt	tttgacaata	tctacaaata	tttcttattt	gtctttattg	ctctttcctg	5400
taatgtttag	tcttcatttt	cctgataatg	gctatctaaa	gttatctcct	caaagaagca	5460
gttattttatt	cacccaaatc	ttctagtcct	tctctggagt	tttctttctca	cttcattccc	5520
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tcacaggtaa	tgactatagt	ttgtgactat	gtaagattgg	attcgttatt	gattttattcc	5640
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cagaatgaaa	gcacactaga	agtaaacaca	gatgtggaag	aggtaaagtg	tccttgaaaa	5820
tcatggaaaag	attcataaag	ggaatgacat	ttcaactgga	ttctaaacca	gttattcaag	5880
ctccacaagg	ttgcacagta	aatgagcagt	ggcaggatga	cataccttag	aaagtaaaag	5940
gaatcttttt	taaactgcta	taaaaatcat	tacatatata	ttttgtaggt	cgagagtaag	6000

Corrected Sequence Listing2.ST25

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gtgctgaata aatctttctt gaaatacgtt ttattgcttt ctatcaatga ccctgaagta	6180
atacagaatt tacacttcag cggttgcaat gctcaaaactt gacaggtaat gcactgtgtt	6240
tgctgatata agaggatga tgtagggcta agtggttttg tgctcattta gctttcagga	6300
gaaaataatt gacttaacat tttgatacta aaacccaaag cctaacagtt aattcttggt	6360
attttaaatt attattgcaa agattattgt gccgaataat atgaaaatat tttatataat	6420
atttaaaaag tatatctctt tcttggtatt atttaaatta ccataaaaat gtgcgaaaaa	6480
gttatactga aatgtgatag gatcttttaa aagtggtgcc ttgattttgt taagtgttac	6540
ctagttttcc tctgaaaaca agaaacatac ccagaagttt tcacgaaatg gtctcatgaa	6600
tatctaaggt tagtccgtag tctcatctga gacaaggaaa gtcccttcca ctatgagcct	6660
gtaaaatcac aagcaagcta gttacttcct agatacaatg ggagtactgg tattgggtaa	6720
acacagctgt ttcaaatggg agaaattggc caaaattaat gggttacagg gcatgcaatt	6780
ccgaaatcca tctgggcagt caaattgtaa aactccaaaa tgatntcttt tgactccatg	6840
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tcctcaaaaa atgggttttt cttttctact gcattgtcag gctgcaaatt ttctgaactt	7620
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Corrected Sequence Listing2.ST25

gtccttattg	tttatatcac	tataaaaaatt	tttgtcaaaag	ccattcaaca	agtctctact	7920
ccaaactttc	ccacattttc	ctgtcttctt	ctgagccctc	caaattgttc	cagcctctgc	7980
ctgatacaca	gtcccaaagt	tacttccaca	tttttggata	tcttttcagc	aatgccccgc	8040
tctactggta	ccaacttact	ttgttagtcc	gttttcacac	tgttgataaa	gacataccca	8100
agactggaaa	gaaaaaaagg	tttaattgga	cttacagttc	cacatggcta	gggagggttc	8160
acaatcatgg	caggaggcaa	aaggcatttc	ttacatgatg	gcagcaagag	aaaatgagga	8220
agatgcaaac	gcagaaatcc	ctgataaaac	catcggacct	tgtaagactt	attcactacc	8280
actaggacag	tatgggtgat	accacccccca	tgattcaaat	gatctccaac	cagggtgcctc	8340
ccacaacaca	tgggaattat	gggaatacaa	ttcaagatga	gatttgggta	gggacacaga	8400
gccaaactat	atcacatgga	tttcttatac	ttttgctttt	aataacacaa	acaaaaaat	8460
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cacaatgctg	agtgtttggt	taggatagag	tcctagaaat	ggtatcacta	ggtcaaacat	9540
tcaaataatt	ttaaaatatt	tgatacatat	tgccaaataa	tctcaaattt	tttaccaata	9600
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taatacataa	aatattcttt	gctaatttga	tgggacagaa	atgttatatc	cttattagca	9720
ttttattatt	gtggttgaat	gactgtactg	tacagccaga	gatatttggt	tcaaaatcca	9780

Corrected Sequence Listing2.ST25

tcttcattat ttactgtatg tgaaaattta ggtgagctat ttaatctctt gatgccttag	9840
tctcctaatac tataaagtgg ggataattgt accaatcata ttaggttcct gtgagaatta	9900
actgaattac tatagaaaat gcttagaatg gtatctagtc accaggaagg actctctctg	9960
tattacttgt ttattatcta acacgtttta ttattaatga agctcagttt cgttatatgc	10020
ttgggatatt tgaaactttt cttagtgaat tttccaataa aattatttgt ctatttttct	10080
atggacaagt tggattattt cttactgggt tgtttcaggt tcagtttagta agaattttta	10140
ggattttcta tcacatttta gcaaaactttt tctgcatttt atctttttttc tttcagataa	10200
tgtttgcaaa atgtaaaaaa aacaaaagggt ttcttcatca agttgggtatc tttatctttt	10260
ttattgcttt gtgatttgaa aattcttgtc ctgagaacca aaatatatat ttgatgaaat	10320
agttctcttc ttttactcat tctgaagtca ttggaattga atttggcata tgatataaat	10380
cctaatttta tattttatga tattcaaaaat ttctaacaaa tatttactta ataatcta	10440
ccaggtttct attgtttctt ctgtttcctt tataatgctt tttctgaagt tatttttcct	10500
agacttaaat attagtataa tattatcata gaggaaaaaa tatctgtag ctatgaataa	10560
aaggctttca tcttattggt gcattaatat atttaaagt agagagcata cagattagca	10620
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ttaaatatgc catttacaat aacatcaaaa tattgaacaa taaagtattt aggaatttat	10860
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aatatatgtg aagagatact catttgtgga ttgagagaca atattgttaa agtatcagta	10980
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tcgaagctga caagctattt ctataattca aatggaaatg caaaaggcag tcaactgcaa	11100
caccagcatg gactgtctgg gttccagtag gttacttcac tactgcctct tctgtcagcc	11160
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tacactaccc tggggaacaa agataggcat gtagtcagcc cacctctgcc accactaggg	11340
cctgaagcct ggcccacctg acactgcagt cctcagcaca gcttcatcac agcttctgtt	11400
aataaccaca ccctaacctt ccaaggaaat cacaatgtc actgacactg tttgtagcca	11460
aagaaatcat agagagacta cattactgca cacaccata atcaaagcca cagtacccta	11520
tccagacaac atcacaggta tatctaaagg aaaaaatttt cccatatgaa agcgaattca	11580
aatataggaa gaagcgactg ttacaacaga tatgcagata aagcttcaac aatatcctac	11640

Corrected Sequence Listing2.ST25

attcaaccag	aagaaagaat	ctcagaaggt	aaagacaggt	cttctgaaat	aatctagtca	11700
gacaaaatta	aaagagaata	atcaaatcct	tcctgacatt	tgggataaca	ttaaagtgc	11760
caaataatcg	aattatagat	acccctgaga	gtgaaaagac	aaagaaaaga	ttagaaaacc	11820
cacttaatta	aataatatat	gaaaacttcc	taagtctagc	aagagtttta	gatatttggg	11880
atgcaggagg	ctcaatggtc	cccaggccga	taaaacgcaa	aaaggtctta	tacacagcac	11940
attacaatca	gactgtttta	agtcaaagat	aaggaataaa	ttctaaaaac	agcaagagaa	12000
agtgtatgat	aacctatgaa	gtaaacctta	tcagactgac	agcaaatttc	tggcagaaac	12060
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cagccttaaa	tactatagcc	cacaaaatta	tccttcataa	atgaaggaga	aataaaaagg	12180
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gaaagtataa	aactccctgg	taagcaacta	aaggagggtta	tcaaattgta	ccaccagaga	12360
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tatataatga	tgagattaac	ccagcaatgg	gaaataacaa	ctctaaatgt	atatgcattc	12780
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gacattttaca	aaacattcca	tccaaccact	gcaaaatgaa	atttgtgtca	tcagcacatg	13020
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caatgtgcct	gaagaaacta	aaaaatcaag	aacaaatcaa	acccaaaatc	agcagaagaa	13440
acacaaaaat	aaagatcaga	aaagaactaa	atcaaataga	gactaaaaaa	atacaaatga	13500
ttaacaaaac	taaaatttgg	ttattcaaca	agataaataa	aattgataaa	ccgctagata	13560

Corrected Sequence Listing2.ST25

gactaaacaa	ggaaaaagaa	tatccaaata	aacacaatca	aaaacgataa	aggagacatt	13620
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gaaaaatgga	aaatatagag	aaatagataa	attcctagaa	acttacaacc	taccaagctg	13740
ttgcatcagg	aagaaataga	aaacctgaac	atatcagtaa	tgattagcaa	aattgaaatca	13800
gtaataaaaa	acatctccca	actcttttaa	agctttggac	caaatagcat	cacagcctaa	13860
ttctaccaat	catgcaaaga	agaataccag	tcttcttgat	gctattacaa	taaatcagag	13920
gaaggaattc	tctctggctc	attctacatg	accagtgtca	ccttgaaacc	aaaacctgac	13980
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aaaaattaaa	atacctggga	ataaatcaag	gaagttaaag	atctctgcac	aaaactacaa	14760
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gatcaaaaga	attaatatca	ttaaaatgac	catacttccc	aaagcaatTT	ccacattcaa	14880
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cagcatggta	tttttagaca	aatggaatgg	aatagaaagc	tcagaaataa	agccatatat	15180
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aatgttttct	acatgttcta	atattttatat	tccattccat	tatacatatt	ccatttctgt	15300
atatagggtta	tatagaattg	gaagactatc	tgccattaaa	agaatgaaa	tcctgtgatt	15360
tcgagcaaca	tggttgaaac	tggagtTcat	tatcttaagt	gaaataatct	aggcacaaaa	15420

Corrected Sequence Listing2.ST25

agataaatat	cacatgttct	cacttatatg	tgggagctaa	taacttgatt	acatgaaggt	15480
ggagaatgga	aaggtaggta	ggaaacagag	actggaaagg	atgaatggag	ggtaggaggg	15540
aagggtgaaga	gaagagagtt	aaaagggtgta	aacatatagt	taaaagaaat	aaattcaatg	15600
cttgatagca	gagtacagt	actacagtta	acaaaatgta	ttatactcag	gtgatgaaca	15660
cctaaatact	tgatcactat	gcaattatat	acgtgtaaca	aaatcactat	gcactatata	15720
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gaacacaatt	agagtaactg	cccccatgac	tcaattactt	cccaccaggt	ccctcccaca	17160
acacatgggg	cttatgggaa	ctacaattca	agatgagatt	tggggtgggga	cacagccaca	17220
ccatttcatt	ccacctctga	cccctcccaa	atctcgtgtt	ctcacaattc	aaatacaatc	17280
atgcccttcc	aacagtcccc	caaagtctt	aacacatttc	agtattaaca	caaaagtcca	17340

Corrected Sequence Listing2.ST25

agtccaaagt ctaatctgag acaaggcaag tcccttctgc ctatgagcct gttaaattcga	17400
aagcaagtta gctacttcct agatacaata gggtcacagt cattgggtaa atacacacat	17460
tccaaacggg aggaattgac caaaaccaag gggctacagg cctcatggag gtccaaaatc	17520
caatagggcc attgtttaaac cttaaagttt caaaattatc tcctttgact tcatatctca	17580
cgtctaggtc atgattatgc aagaggtggg ctcccacagc tttgggcagc tctgcctctg	17640
tggctttgca gggtagagcc ccactccagg ctgcttttac aagctagtgt tgagtgcctg	17700
cagcttttcc aggcacatgg gtgcaagctg taggtggatc taccattctg tgggtctggag	17760
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ctcttgagaa cagcatgagg gtaacatgt ccatgattcc attacctccc aacgggttcc	19140
tcccatgaca cgtgaagatt atgggaacta ctacaattca agaggagatt tgggtgggga	19200

Corrected Sequence Listing2.ST25

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agttgacttc	atatgtgatc	taaatacatt	accattattt	tggacttatg	atgtagctct	19560
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accatcgtgt	tagagttgcc	tgcagtattc	agtacagtaa	catgctgtac	acctaggagc	20280
aacaggctat	accacatacc	ttaggtgtat	agttagggtta	taccatctag	gtttgtataa	20340
gtacactcta	tgatgttctc	acaatgaaca	aaatcaccta	atgatgcatt	tctcaaaaca	20400
tgtccctgtc	attaatacag	tatgtaacaa	tacagttagt	acaatatgta	atacatgact	20460
atattcagaa	tttttagctat	ttctcttata	tttcaaagtg	attttcttat	gcactgtgtg	20520
gcacgggcat	ttcatttttag	taaccacagt	ctgggaaagg	agaagtcttt	gaaggatgtt	20580
gagcaagggt	atgacatggc	cagatgtgaa	tttttgatca	gtgactccat	gttagcagat	20640
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cttgggtgatc	aaagaataat	gagactcatc	caataagact	ctgtgaatga	ttgaatgtag	20820
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tttgattttt	agaacaaaga	ataaatttgt	acatgcttta	tgattcctgg	ttgaattttt	20940
aaggataaaa	aagtcagctg	taatattatt	ctttcctgat	accatgcagt	atttgtatca	21000
gtgatcttat	tcattccaca	cacattcttc	ttgaacctgg	acactgctct	agacactgat	21060
tctttccaaa	tatcagataa	ggttattctt	acgtagaccc	tcagttcata	taaatatgat	21120

Corrected Sequence Listing2.ST25

tttcccaaaa	tgtgaaataa	gtgacttttc	ataagatatt	ttttaaaaga	atgtcttaat	21180
aataaattgt	gaatgttgca	tggaaatgta	ggtgacttgc	attgtgcatc	ctgtgtttga	21240
ttcactgctc	ttgcatgtct	tgccttttagc	tgggatgaca	gcagttcagt	gagcagtggt	21300
ctcagtgaca	cccttgataa	catcagcact	gatgacctga	acaccacatc	ctctgtcagc	21360
tcttactcca	acatcacctg	cccctctagg	aagaatactc	aggtgagaat	taccaccttt	21420
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agcacaagcc	cttaatccaa	aattattaca	gaaactggaa	aatgcagaga	taataaggac	21540
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cccttaggag	gagcaacaat	gtgcactgca	gccaattttg	aataaacaga	agcagcttat	21660
atatatatat	atatatatat	atatatatat	atatatgata	tacattacat	atztatatat	21720
atgtaatata	tgtgccatat	agcctggtgg	tatagttatc	tatacaaata	tattttattta	21780
ttgttaatat	atagagtata	taaatatcta	tttatataat	agatatattat	atatattaaa	21840
tatctattta	tataatagat	atztatatat	attaaatata	taaaaatata	taacatataa	21900
tagatatata	ttttatatat	tatataaata	tatatattata	tattttaatat	attaatgatg	21960
aattactata	tttgtataga	taactacacc	accaagctat	atggtgtgta	tatattaata	22020
tataatgtat	aattctatat	taatataata	gtaacatatc	aatacttaat	ataatatata	22080
ttcaattgat	tacaatctaa	ttcagaaaga	tttatgttgc	catatctctc	cttacaatat	22140
cgatatgttt	gtttaaaaat	ccagcaatta	ttttcatagt	ctaatttttag	atagttcttg	22200
attaatttta	tatgatctct	gaaatatatc	actggatctg	ttgtgaatga	taaatcaaaa	22260
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gatatagaaa	atctctacct	ttctgtagcg	tttaattggg	gttttctgca	tgtattttatt	22380
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gaaggtaaat	caaaatagaa	tctttggatt	tatccagtta	tctgaaagta	catttcattg	22500
ccttaattca	cactttataa	atttttctac	ataaagtttt	tctgtaatat	ttgtctttat	22560
agctgaggac	agattcagag	aaacgctcca	ccacagacga	gacctgggat	agtcctgagg	22620
aactgaaaaa	accagaagaa	gattttgaca	gccatgggga	tgctgggtggc	aagtggaaga	22680
ctgtgtcctc	tggacttcct	gaagaccccg	agaaggcagg	gcagaaagct	tccctgtctg	22740
tttcacagac	aggttcctgg	agaagaggca	tgtctgcca	aggaggggag	ccatctaggc	22800
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gcaaaagtgc	tttactttat	tgtttccatt	caatctttgt	tttctctaac	aatagcattt	22920
ctaaaatacc	aaattcttat	ccatattaaa	catggagtca	aatagttaaa	tagtttttct	22980

Corrected Sequence Listing2.ST25

gtctacgttt cacaaactcg tcatagaagc ccaagtaggg cctatatcta ggcattctct	23040
ggaaagcctc ctcataaact aggggtactg gatgccttac cttgccagag ttatttcagg	23100
taatggggaa ataagattag gttgctaaag caacagttaa gttttttgt ttttgttctg	23160
cgttcttaat gaaagtttgg aatttttaca ctaaatatgc cactgaattg cactacagac	23220
tctgagagga acaagcaatg acactaatca attggaatgc tggagatttg aaatattgtc	23280
tgtgtattag acttcatgaa agaagagaat gaaatagttc ttcaaaattg tgccatactt	23340
tttttaaaaa gactctcccc gtatttttaa aataatgcct aattataaat agtgccacct	23400
gaagcactaa ttaacagggt actccaaata taatcatctc acagatatcc aaatgaattc	23460
tttttctagt aattagcttg atagggttaa gtgttacctt tttaaaaaga gttgcaaaat	23520
ataagacatt aacaaatagc aaaacatatg ttttcatttt atctcttcca tctctcataa	23580
tgtttcttct gacagccaaa tttttgtagc tatgcactca gtcctctcaa tatatgagat	23640
ttttgatcta agccaataca tttaggaagg gaaataatat aaagaagcat tcacatttta	23700
cacattgttt cacgaagtgt ggtgatatca aactctacag gcacatatat ttgtgtattt	23760
ctccttaatt agggaaaacc gatgatgcca aagcttctga gaaaggaaaa gctcccctaa	23820
aaggatcatc tctacaaaga tctccttcag atgcaggaaa aagcagtgga gatgaaggga	23880
aaaagcccc ctcaggcatt ggaagatcga ctgccaccag ctcttttggc ttttaagaaac	23940
caagtggagt aggggtcatct gccatgatca ccagcagtgg agcaaccata acaagtggct	24000
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gaaaaaccag tttggacggt tcacagaatc aggatgatgt tgtgctgcat gttagctcaa	24120
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ctggccgagg aggccacaga tccagtacca gcagtattga ttccaacgtc agcagcaagt	24240
ctgctggggc caccacctcg aaactgagag aaccaactaa aattgggtca gggcgctcga	24300
gtcctgtcac cgtcaaccaa acagacaagg aaaaggaaaa agtagcagtc tcagattcag	24360
aaagtgtttc tttgtcaggt tccccaaat ccagccccac ctctgccagc gcctgtggtg	24420
cacaaggtct caggcagcca ggatccaagt atccagatat tgcctcacc acatttcgaa	24480
ggtaaggatg tataaaatga tgctggaaaa atataaagga taaatatgtg ttagacacat	24540
acattacata taaatgtgtg tatatatata ttttaaatat gtataaggta tataatatat	24600
atatcttaga attctttaaa gtacacagtg agctctatga agcttatcat ataaacagct	24660
agcaaaaaaa atagttctca ttttgagaaa cagtcaaact tcaaagtttc actgtcattg	24720
tgatactagc aacacaaaca tctaagagac ttaaagctg atggtaatac ctaagtgtag	24780
tgataaggca aagtaatagc ttgtaaaatt tctatagatt tccattcctc cttttcacat	24840
taaaaattaa aaccaaatag gttttcatga cttttggcat tcatttccag tgtcattttc	24900

Corrected Sequence Listing2.ST25

ttgctggctc ttaatgagtt ggtgatcata aatgtagatg aagttgtttt ccttgtaaca	24960
gattccattg gacagattta tacagtgtca tatcttgaca cattaaagac aatcaagata	25020
tgacataatt tgaaactatt ccagtgtttg gtacagtatc acaactgaag agtgggctaa	25080
gctttctaac tcttcattctg ctttctttga catgactctg gtaaggatca tgacttggtt	25140
tctgttcctg gattgttttt ggtgttaaata atgtgaagtt ctgctctaag atatcactgt	25200
ttttaaatat ccatgtgttt ttaagtggta ggaaaataaa tgcagttaaa aattggggac	25260
aaatatctaa acctctctga gtctgttttc tcatctgcaa aatggtagag tgtggtttat	25320
agttcattat gggttcaata ttttaaatgt ttgtttttat tctgttgact aaaccagaa	25380
ctttgatatc ttggaaagga aagattttga aacattttatt ttacaataaa gcaatttcag	25440
atacctgatt gtttgaaaaa cctaaaggct ttattcctcc gtagtaatat taatgctgca	25500
gaactgtctt tttaaaatac tgattctcat tgggaagaat gaattatggc gtatagggag	25560
agtaaatatt tctgtttctt aagtaaaagc caatagtgcc ctctgtggc ccattaccta	25620
tgaacaatt tctcatattc gtcataaaat atttactgt aggaaatatg gatttcattg	25680
caactcaatt agtaatcatt atgccattac ttcatatcat tgtatttcca tatttacata	25740
aatttgattc taccatctgc ttcatttaca aaactaaaat gttttctgaa ctaaactcca	25800
aaatctaaca gcaccagctc tgtttcaaata cactattaaa aaatgtattt gaatagcact	25860
ggcaactgac ataaaaccct ttggcctctg ctggggaaaa tacagacaaa ctgacttggt	25920
gccgacaata tcaatattgt ttccaacca ctgctccctg acagtgactc agaccaccag	25980
atactcaaca caactcccata aacttgcttt aagcgttcca tctagatttt gaataaactg	26040
tttaaaaatt taaaaataaa aaaaaagag aagagctcat ttaagtgttg tctatcgaat	26100
gcgtagaagt tgtttcatta taatggttct gtaaataagg aacagcaagt atgggtcaa	26160
tactgacttt gagtgaaggt ctcatgatca cttaaattat gaaaaccagg ggttttcatg	26220
tttgacttac tttgttcca cccacttccc ctctttccct agtagcagct cagtactgac	26280
ctacccttat atgagagatt ttctgcactt gataaagaag tccaagctta taaaagttca	26340
ttaacataga gacaggaagt gctttgtagt tcagtacatc aaagcacact tggctctgtg	26400
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tactgagggg gtgaaatctt cctcagtaat gccagccct agtaccacat tagcgcgga	26580
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cggcagcagc agccctctct tcaataaacc ctacagacta actacagatg ttataagctt	26700
aagtcactcg ttggcctcca gccagcatc ggttcactct ttcacatcag gtggtctcgt	26760

Corrected Sequence Listing2.ST25

gtgggctgcc aatatgagca gttcctctgc aggcagcaag gatactccga gctaccagtc	26820
catgactagc ctccacacga gctctgagtc cattgacctc cccctcagcc atcatggctc	26880
cttgtctgga ctgaccacag gcactcacga ggtccagagc ctgctcatga gaacgggtag	26940
tgtgagatct actctctcag aaaggtgagc tttcctggag gcattgataa catcttcccc	27000
ctcttccctg cactatgcct aacccccacc ccattaaatt cccttgattt cactgtgagt	27060
gccccggtgc aaaaagatgt aagactgatg aaaccgggccc tttcatttgc tctcattacc	27120
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tccttatgat gacttaagca ttttgaaaga ccaaattgaa attattctat agttatgctc	27360
agagcaatat gttaaatttg ttccatttgt acttctatga aaaaatagca gatggattgc	27420
tgggaaatcc tagttggcct ggtaaaaaa aaaaaaaaaa tcaattgtca gccatgaatc	27480
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taaagcttta aacatgggtc tggccacatg tggaaagaaa tactgggtcac gtaaaatacc	27840
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cccagagcaa aacattgctt ctttccctct ttacttccta cttgcctaac aatgagacag	28140
ggacagccgt gcaaattgggg ctttccgatg ataaagtaat tttaacacta actaaaatat	28200
tggtgtttcc tatggtgggc tgctaattac aaaatacatt tttcctccta aagaaaaaaa	28260
ctgggccaag gcaaacagct cagtgatagc aaataaaatg taaccatttc cctatggttt	28320
tgctgttata tgctattata gacagcatac gtaaagacca gtaagggttc atttttccac	28380
ctaaaatgtc gggcttcctg taaaatcttt gattctagtt tcagcacttc taaggtaa	28440
gggcatcttc acatgtcatt tataaaactt ctaatgaatg aattatatta aaatagataa	28500
acaacctata gttttaatga atgtatccta gattgtatgc tcatatgtaa ggattctaaa	28560
tatcaacttg ataaccaaac caaacatagt gcaaataagg tatcatttat taaccacaac	28620
caccttccac aaaactgggc attttttaat tattaagata atctgcaaca agttggccat	28680

Corrected Sequence Listing2.ST25

ttagccatca	gcctatcttct	tcagcattta	gacattaatc	ccagattcag	aaataaagtc	28740
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gcatagctat	aaccaaaatg	cagttttaat	attttactct	aatctatatt	ttaactgaag	28860
tcaataaaat	tttactatg	gaaatacact	agaaaaatg	caattttcta	ttctttttta	28920
gcagatttat	ttattgtaca	tggtcagtct	ttgaaatagg	ccaattttat	ttatgttatg	28980
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gccacctgag	tagctggggg	tataggagcg	gaccaccatg	ctgggcta	ttttgtat	29160
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gatttgcaga	aattgtctat	gttagaaaat	cattaatatc	tagattcaaa	catatttcta	30300
aataaagctt	taaattatta	tggtaacttt	aaatgtat	attctaattt	ttttcattaa	30360
attgctcttc	atcatataaa	tatataattt	ttatacaact	ggatgagttt	ggcagaagaa	30420
taccaacttt	tcatattctt	tgtggcatta	aactttaact	tgtacacatg	gaaataaata	30480
atccttaaaa	tgacttatga	ccacataaat	gccttagcac	atgtggttca	tatttg	30540

Corrected Sequence Listing2.ST25

tttctcatat ttgttcaata taatttattt tgtttgttta tccacagtac ttaagaaaac	30600
ttctatagtc aacatatata ctgtaactgg cctctacaca gtataagcaa ttaccttaca	30660
tggctattac cgataaagtt aaagttgtat aaagcctttg gatgcttttg atttcagtg	30720
taaataatgg agtacacata gaagaaaaca ttttagcttt ggtttgagtg atcaaatttt	30780
aggtcagcct ttttacattc atgttatatc atccccatta tgcgtatcct gtgtatttaa	30840
ttttgatcat ttgatgtcct aaaggaagaa agctataatt ctgcaatttt aattaatttt	30900
acactttgct tatccacatg ccagagatta taaaagaaat ccctaaactt gtcccaacta	30960
gttgttgata tcctcttcct gtatttttag agaggccatt tcttattttc tctagacata	31020
gcttttcatt ccttcttggt accaattgtg aattccttaa aatagagatg ataaaattta	31080
tagcctttta aataccta attatgatttc taaaagatgg tatagcttaa tttcattaaa	31140
atattcaa ataatgatact agaatacaatt aagttttaag caaacattca tatatctttc	31200
ttcacatgtg taaatgggaa ataaacatgc ctttttatta aaaataattt gaagacaaaa	31260
gataagtatt aaacaacgtt ttataccatc tctgtcaatt ggaagttgtc actctaactt	31320
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aaccattttt gttggatgtg taatttggaa gttttgttta cattatgtcc ttagggggtt	31680
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ctgctatcag atcaatttaa atctgaatta atctaataat atttaataat ctcaaaataa	32400
ttattccatc cataataaaa aataaaataa aaatttaact tatggccatc ttttactgtg	32460

Corrected Sequence Listing2.ST25

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gctgccata	tgtattccat	ttccctatgc	cttctgtgac	catccttcat	ttcccttggc	32880
cctggcccac	cactgtcctc	catttgtagt	ccatgttttc	accctcttta	catcctttct	32940
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ctatgtgatt	caaacagatg	gcgtaagatc	atctggaaga	actgagcaat	tataattaga	33120
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catcttctgc	agctggaaaa	taccactttt	ctaacttggg	taaaatattc	taaaatattg	33420
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caacacgttt	tcattttaaag	ggaggggataa	aagcacttta	acagtacctt	tcatttgtgt	33540
cattgtttac	tcttcacaga	aaaatctcca	aacattatgc	tatttattgc	tcatgacaaa	33600
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atttaataga	ttcaatgact	ttaaaaatat	atttattttc	tataaagtca	catataaagt	34200
attttcatta	ttttatgggt	aaatatTTTT	attattagtt	tatcagaaaa	acttgtacat	34260
aaagatgagt	attgatacat	aatcttatta	gagccagaga	cgatcattcc	ttctagaaaa	34320

Corrected Sequence Listing2.ST25

acacatctct	gaatttagga	cggaggacaa	tgaacaaga	aatttcactt	tataatttac	34380
ctttgtcaaa	ctatcccaga	gcacatcaat	tccatcatga	aagtactctt	ttgacattat	34440
ataaaaaatt	agtaatagaa	aacacacaat	ccaaaacctt	atattttcta	aacttcaagt	34500
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gaactcaaac	accatataca	tttgtaatga	ggcacaacag	tcaattttga	gccttgattt	34620
ttccagggtt	tagctgaata	atcttcactg	ctttcttagc	tttttgccag	tctagtttgg	34680
ggactatttt	gccttactgg	gcctaaacag	agtgtaatat	taaaatatgt	taataagcca	34740
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attccatgaa	cacagggtgaa	tgaatgcccc	tagtttctct	gagttggaca	atttcatgcg	34860
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gaaagtgagt	ttactttgtc	tccatattct	ttttctccat	gctcgggaat	cccctgcttt	34980
cctgatccca	ccacaaaaac	tcccctgagg	atgaagcctt	ggctttccag	gcttccaggg	35040
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aagtgtcata	agcttgctaa	gtacttcatg	tctcctatca	attctttcat	taattgacgt	36120
taatttgatt	agttgactcc	ttcttctatt	tttcttcacc	attattattc	tgattaaatc	36180
caccttcatt	attccttagg	aacaaaaaga	ctcaccactt	aactatgtct	gacattgggtg	36240

Corrected Sequence Listing2.ST25

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gtaaagaatg acggatatag tgtatgtaaa gatggagaag tgtgtaagac ttgacagatt	36360
ctgccaaatc attattttca ctggaaagca tgtcttacac gatcatagag tagcattcat	36420
cagatatgcc tgagctttgt ctacatttaa ttgagtagta attcgcaaca cagtaaccac	36480
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caaaactatg acattgttat caaggactca tttaccacaa atatcaaata tttgtgcaaa	36600
gataagttta tgctaagatt tgcataaatt aaagttaaca tggcaactga agctaacatg	36660
tccatgggtca caatgtgtta aaaaatgaat ggttctgtag cacacttggg aatgtatttt	36720
attacatagt tttcagagtt aaaacacaat taataaatga aatgtgaatt atacttttac	36780
tgacaacaaa gctctctgta gagctttaat gttctaataa attagaaaac cactgatcaa	36840
atacatccct tacatttcat tgctatagaa accaagtctg aaagggttaag tttacctttc	36900
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acaattcttt ctcttggggg tgctcatctt aacatagctg tatcatttat tgtagacaca	37080
aggtcacttt tgagagtga tgggactata ttaataattg ttccaggat taggtgcaaa	37140
ccctgggcaa tgcaattcat cctccatctc ctcttatat ttatgtgttt accaagttgt	37200
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attctaattc ctcaaatac catttcactt tctgtctgag acctttttca gctctaaaac	37320
taaaatccca tcagtgtgct agaccatata gccacctgaa atcaaagtct tttcttaagt	37380
tcttttcttc tatttgcctt ataatttcat gtatcatcct tctctctact ctagcacaaa	37440
atctgtgtaa tcaatagtct tacttgaaac tgtgctcttc atattgtaca ttttcaatag	37500
acaggaacct gtgattttat cttcagaata tctcctacat ctgtctctca ttttcaggga	37560
cattgtcctt gctgaagctt ttttaactat agacaattgc agcagatttt aaactgatct	37620
tactctgtcg actcccttat gtttcaacat tttcacccat tggaaggat aaaagaagat	37680
attcctgtcc gtgtcaacat aatctcatgt acctctccag atcttagaaa cacgtatggc	37740
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attcaaaaac ataataattt aagagttttt attgtattta cagttcacct gaacctctgt	37860
tcattgggca agaaaatgag tactcttaaa atgcaataat aaattaaagt tactttatta	37920
ttaaatttta aatatatata tatatactta ccttaaatat gtcctcttgt tgtcttttag	37980
catcacccat ttttgatttg accattatct tttctgaata atcagtaaga tacaggatta	38040
ttattaatgt tcaaaagttg cagtattcat gttttcttta ttctttctac caattaaaat	38100

Corrected Sequence Listing2.ST25

gtgttaatat ataaaat	tttt tagaaat	tttt actataa	aaaa atcacaac	at atattaga	aaa 38160
attaagatca ctacaatat	g tcatat	tttag tagactact	g tgagctact	g ccacagta	aaa 38220
ctatggttcg tgtgtcg	tcc cagcatg	ct agccctag	ta gaaaccatt	c ccattca	aga 38280
aagactaaca aagtatag	ct tacataa	atc aaaaagt	cctt tggatga	aac ttcattt	ggg 38340
aaaataaccc aatcgct	acc cttcaat	ttt ttatga	atga aaaaat	ggaa gaataa	aggc 38400
ctctaagatc cattcaa	agc caggaga	cac acaaga	atct ctaaata	gaa gagaa	acaga 38460
agaggtcata gttctt	gtga gccatct	cat aacctg	gtga gactcatt	gt catgcct	cca 38520
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ttttgcatat ggtgatt	gtt aaacac	ttt gcatag	gaac agtttct	atg cttttg	tact 38700
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aatgaactcc tgtctt	ctat tctttc	ggaa gcataga	atc tcacgg	tcag aagaga	ccac 38820
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tggcactgca tactcc	agcc tggaag	acag agtgaga	ccc tgtctc	caa taatag	tatt 39300
taataatatc ataaaa	accc agtccac	att tatata	ggat cctgt	ttttc tcaagt	tact 39360
acaaataaat atata	atctt aataaaa	agggt tagtgg	cttt gccaa	gatag tggctt	ggct 39420
atgcaaatgc aattta	agac aaagtt	ggta gccct	ctttt tccta	ataca ttgcc	atatc 39480
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ccaaagcaga tggaa	agcaa aactacc	act agaag	ctctt tacca	atttg tgttcc	attc 39660
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caaaaggggt tgtaa	atgca aactatt	ccc tttaaaa	atct atccta	atcc tcatta	atgt 39960
ttcatcttga tagag	ctaag tattat	gtat tgaaat	tgta gaagt	acact tcactt	ggat 40020

Corrected Sequence Listing2.ST25

atctctgcaa tcatttaggt aagaattata caaagccaaa aagcaaataa aatatcctcc	40080
taaccctata gatacgata ctaaaatgat gcacttgcaa atttgtttaa tacttcatta	40140
atttaaaca gagtaaattc atactgtgaa ccaagaatag ggtgacttac cccaatcttg	40200
ccaccttaaa cataaacatt ttaagtcttc aatgtcctac agtgtaccta ctggctgttg	40260
tcactaatca gaccgaaatg gtactaatgg tctactgcagg ctgaaggaat atgcttgaaa	40320
gataggcaga tcctctccct ctcccttttt tacttttttc gcctttccat cctttcttct	40380
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gaggggtgtt ctgtgtgtta attcggttaa taccaggatt atcaagcaca gtgccttcca	40560
aatgtgagat acttctctcc gggtacctct ggggttactt ttctgtttt acattgtttt	40620
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cttcataaca ggtagcagaa aacaccatgt tattacattt ctagcaagag cagtagaggt	41460
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gctcaaacag catcccagcc caagactctt ctttcgatct ctatgatgac tcccagcttt	41820
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Corrected Sequence Listing2.ST25

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actagtgtaa	ttatcatttg	ggaaactaga	agcttgaaga	agttttattc	tgtattatct	42060
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Corrected Sequence Listing2.ST25

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ctatactatc	attttagtaa	tgacgagttg	tccatgtttt	gttctttgag	ccgtgactgt	45240
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atcgaagggt	aaaagcagta	agggtaaagg	gtaaaagcat	aaaagaacca	gagatgtttt	45360
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attttattat	ttattttatt	ttgagtcgag	gtcttgcttt	gtcaccagag	ctggagtaca	45480
atgacacaat	catagctcac	tgcaaccttg	aactcctggg	ctcaagttat	ccttctgcct	45540
cagcctgtca	agcagctagg	actacaggca	cgcaccacca	tgcccagcta	atttttaaat	45600
tgtttttagag	acaaggctcat	tgctatattg	accagactga	tcaataccca	tggtttcaag	45660

Corrected Sequence Listing2.ST25

caattcctcc	tgcttttagcc	tcccccaagtg	ctgggattac	aggtgtaagc	cagcacactt	45720
agatagaaac	tttattttatt	aagagaaaaa	taccagtgtt	tcaagttctt	ttgcaaacgt	45780
gtgacattat	aattcatttt	tgacaaggag	agtttttctg	tttggtaaat	acaatttctat	45840
cttttttaaa	aaagtagcct	acaggaagtt	atattttatg	agtgagtcct	tttagagcta	45900
ggttaacagt	gaggtatatt	taaaagcagc	ctactgaatc	tcaatgggac	ttgagtacta	45960
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tgatcaactg	agcatcatgg	gcagtatttt	tttactcat	tatcattagg	ttcaaagtgt	46080
tgtttgaacc	ttctctttat	agattaatct	catatattta	ctgccttaca	tagtcattca	46140
aaatctgact	gttattggca	gaagtaatat	ttttctaata	tctcctttca	atgattaaaa	46200
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gtgcaaattg	ataaagtgg	gaatgtgtaa	acacacatga	aaaaaacaca	taaaagaaat	46320
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ttattctaaa	tacatacaat	aattaatatt	tggataaagc	taccttcatg	aaacctaaga	46500
aaaactaaat	taaaaagaaa	gaaagaaaga	aaaatacact	tagatagaag	aaataaggtc	46560
tagtgattgg	tagcacaata	gagtgactat	agttaacaat	aattttattgt	acatttcaaa	46620
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gaagaatggg	atattccact	ttcccagatt	tgatcgttac	acagcatatg	tttgataat	46740
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gaaaaattta	ttcctcaaga	aaaggatcat	gagtttaaga	aaaaacagat	tactagtcta	46860
ccagtgtcca	gtagaccttt	ctgtgttaat	aaaagtgttc	tgtatctaca	ctatctaata	46920
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agattggata	gtgcaagttt	atagagaaca	caaggggtac	atttgtagat	aggagtggga	47100
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tatgaaatgg	gaacacagat	taaaatagag	tatgtatata	tatacatata	tatgtgtata	47220
tatatacata	tgtatgtgta	tatatataca	tatatatgtg	tgtgtgtata	tatatatatt	47280
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ggtgatcgag	ccacatgaga	aggtgatatt	attagaaaat	tgaaagtgtg	atttgagatg	47400
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tatttgggga	actacttaag	agaaaaatca	taaaacatga	ggagtcattc	tttccccagt	47520
ccgccatgat	caggccttag	gatttaattg	gcaatgagaa	aataacctatg	aaaatgcttt	47580

Corrected Sequence Listing2.ST25

ttaaactatc	acatgaaaaa	gcaatttatt	atctttcatg	ccttcttaat	aactctcaat	47640
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ggcaagttag	caaatttctt	tggactatac	ctataaaaata	aaatttgaaa	atattagcta	47760
gatctaacc	atgtgtctcc	ggatgtctgc	aaagtgggtg	gaaatcacaa	gcctaacctg	47820
atctgcagag	gtgttacctt	tggcaaactt	atggtttttg	tgtttgtttt	gaaatctaag	47880
gccaagcgcg	gtggctcatg	ccggtaatct	caacactttg	ggaggctgag	gcgggtggat	47940
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aaaatacaga	aattagcccc	gtgtagtggc	atacgtctgt	aatcccagct	atttgggagg	48060
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aactatattt	aacctgtttt	gaatttgaat	tctaaattgt	atcttttcat	gagagcaagt	48720
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gtcataactt	tttaattagt	aaatttgaat	ggataaatgg	ccacttattg	gcttatagaa	48840
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gggcttgctc	aaaaccattg	ttaaaaaaaa	aatggcaa	aatccagttc	catcatgata	48960
tcattaatcc	cacacctaag	ctactgaaaa	aaatatatta	atattctggc	tcattgcttt	49020
atcttttatg	taacaccac	ctggtattaa	taaccacaga	gtacgaaaga	aggcaaagg	49080
taaagcaa	aatagttttg	aaaaattgg	agtgaaaaa	gtcatgctat	acggtatgta	49140
tataatagat	atttaatgat	tatgcttgct	actagtatat	gtaacaggac	tattatagat	49200
taacaaaaat	gcggtgagta	tatttcttga	ttatttttta	aaagaataaa	ttattattta	49260
aaaatacatg	aattatttat	tgattcttga	atctttacca	gctttctata	attctaggaa	49320
gcctagaagc	agaattgggc	aggataaact	ggcaaaaaat	gtaaaaagta	ggccgggcac	49380
ggtgggctac	agtgagtcgt	gaatgcgcag	tgcacctgag	tgatagatca	agatcctgtc	49440

Corrected Sequence Listing2.ST25

tcaaaaaaaaa	aaaaaaaaaaa	aaaagaaaaga	aagaaagaaa	aacaacaaca	aaaacaaaag	49500
caaagtacta	gggaaaacta	atagacatag	ttacatagtt	aattgtgcca	tatgttttaa	49560
ggcaatgaaa	cttttatctt	aatattcctt	gcttactttt	tattcaaaaa	ccaaactgtg	49620
tataaaacct	taaaattatt	aggatctaaa	aaataaaatc	tttccttaaa	aatctaaaat	49680
tgagatgtaa	attattcaag	agtgcctttt	aaaacagttt	tcttataaag	gctattagga	49740
ttctaccact	tagccacttt	attatttagc	cactatatta	ctaagtttac	atatttttaa	49800
aggtagtgaa	aatatagggg	agacaaagct	cagggttaaaa	gagtttctgg	caaataaaat	49860
atatcctgat	ggtttagacta	ctttgcttta	tgttttctga	aagaaaagca	gtaaaaaaca	49920
gttcaggtag	ttttgtgtca	attaatctag	aactatacca	aaagtagaca	tagaaaacga	49980
gagattgttt	ttcagctttg	gatctgctta	tggcaataag	cagacttgta	ctattcaaca	50040
acattatgca	ttcttcaact	tttcccagaa	taagggagct	tcccaaatgc	aatgggtgcac	50100
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gtaagaccat	ctacacagga	taatgggtga	aacttgggca	ccaagcctcc	acaacacagg	51300
atactagcat	ctcagactat	ctgttttggtg	tcattatctt	gttgccctcta	actgccattt	51360

Corrected Sequence Listing2.ST25

tatgtgtggt gtgtcaccta ttgttctaata cacatatatttc acaaatacat atttggttgc	51420
actcgtgagc aaatcaaact gcattcagga aagaatacta ttttaatttc ccttggtaaa	51480
acatttgtcc tggtaaaga gagcaggagg actttaatta tgactttatt caaggtgagg	51540
taatggctgt ttgattggtt tacactgagg caatcagaca acagagaaaa aaaatgcctt	51600
aacaacagct tttgcaaaag tattcctttc ctttgaagtc ttattttatt agcctttaaa	51660
aataaaattt gtgctatgtt taaaaatatt tgaaaattat tgattaaacc aatttgcctt	51720
tataatctct gaaccaaaga gtggatatga tttttaaaaa tcaaagtggg tttatttaca	51780
tcacatggac atgacaaagc ttctaacact gatcatagta tagctactga agcatcgaag	51840
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tcagtagtta tggtttaaaa aaacaatttc aatcacttta cagtttcctg gattatattt	51960
taaagatact ggaatcatgt aatagagact atttaatttg agaaatgctc tttgagtttg	52020
gattcattta tgaataaaat agacgctgta ttttctgaaa tcattcatag tcattatctt	52080
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gacagcattc caaaagtta actacaacta tagataagat ttgtttttga agaaatgaga	52380
agcatcaaaa gtagaatgtt taacatccaa gtaactgaaa tcccttgaga ctagatatat	52440
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aaaaaacct aagattttct gaaaaagaac atggagtatc ttttactaaa aaagaacaag	52980
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acagtttttc tagaaggaga agaatacaata cagagggtaa actgctcttg agtcatttgc	53100
catttgaggg atggcaaatg gagcaagtga gcgtactttg atttgtagat tagagtttga	53160
cacataacac tttgcttttg aatgacattt gcttggttact gtggagtcag tgttcatatc	53220

Corrected Sequence Listing2.ST25

ctttattttc	aggagttgct	gctgatacaa	tggggttaga	atgagctaaa	tacagcattt	53280
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Corrected Sequence Listing2.ST25

cttccacaca	cacacacaca	cacacacaca	cacacacaca	cacacataca	cacacatacg	55200
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aacattttta	taatattggt	ataactatgg	gggtaaaatt	ttgtatatat	ctgaacattt	56940
ttgttcttaa	ggaaataatc	atttttacat	atccaggaat	ttgaattact	ctcaagtcac	57000

Corrected Sequence Listing2.ST25

ctattaatta	caagtcattt	tgaactcatt	cattttcttt	gtgtttgctt	tataatgtca	57060
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caagtaaact	ttctaccttt	tggttaaatg	tgagtgcagc	ccccacagtg	agaaattggt	57420
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aaataatctg	ttggttttta	caacattttt	aagtatcaga	tattcatctt	tactcagtat	57540
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acttgtattt	taatttttaa	atttgaaatg	catctatgtc	tctgttaaaa	tgcatttctt	57720
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tcataacata	catatataaa	atactatatt	atatatactc	taggtataca	tatatgccta	58740
tatatgcacc	tatatattta	tatattacta	tataatatat	agtatatatt	actatatata	58800
ctactatata	ttactatata	atatatagta	tatatatagt	atatattata	tagtaatata	58860
ttactatata	atatataaat	atatgtgtgt	atatatatat	atgcctagag	tgtttttaat	58920

Corrected Sequence Listing2.ST25

ttgtcagtg	gctgtctctg	taatctatat	gaagaaataa	aatgtagacg	ttatgtataa	58980
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aaaaattttc	ccttatttgc	ctccttttcc	atttacccta	ttgagtgaga	aatttagcct	59460
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Corrected Sequence Listing2.ST25

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ataagttttt	ttgtgcataa	ttacaaaactg	ccatttcta	cataaacatt	ttgtggttac	60960
ttatagctag	aaaatgtgag	taatatagtt	tatacagcat	actctttaca	atccccgattt	61020
ctttgtcaaa	ctttaattca	tattaaattg	ataaagtata	cacaaaggg	aaaggagagt	61080
aattttcttc	aagtttcaca	tttaaggatt	catagtagaa	tgattaaacc	ttacatttct	61140
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ttctttgtat	ttttgtgatc	catttgatag	taggtgcctc	agcatttcca	ctctgctata	62640
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Corrected Sequence Listing2.ST25

tttttggcca	aggatttcca	aattttgccc	catatatagg	tatagtttat	tatagacttc	62760
gtttgcaaaa	tattaaatcc	ttatatcctt	ttagggacac	aataaaattt	tataagtttg	62820
agataatgta	cttgcagttc	tacctcaggc	cgtggtgaga	gattgaagtg	cctcttcatt	62880
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gagctttaat	aaaatcgtca	aatacttctt	aatcttaaga	gttatagtta	tgtactacaa	63000
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Corrected Sequence Listing2.ST25

ctatgaaaca aaggccaatc ctgtgtaatt ttgaaataac aagaactagt tgccatctag	64620
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ttaaaacaga atgaatagtt caatgaaatc aaaagagtaa atcgaatatt cttataattg	65220
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tggtataatt caaagacaga atctaattaa aaccagtaga ataatgtata taacaatata	66420
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Corrected Sequence Listing2.ST25

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Corrected Sequence Listing2.ST25

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aatccatata	ttgatggcat	atacattttt	cagttttttt	tctaaatgat	taatgaggat	69960
tctcaaaact	tgagtatctt	ctatgtttcc	cttcaacata	aagaaattgt	atgaaaatat	70020
tttaaaaatt	tctaattgatt	ttatagttag	ctatcttggg	aattcatttc	taatcatgta	70080
cctcatccaa	actccccact	atggacaaaa	ataaaataaa	aattattagt	tgcatctgaa	70140
ggccacatta	caatttctat	gcattataga	aacctgagaa	aatgtatctt	aaaaaataaa	70200
tgtgaacaac	taaccataat	tatgaagaag	aaaaatgaaa	actagaaata	aactattgaa	70260

Corrected Sequence Listing2.ST25

aaatgtctat gtatcagtta agtttttatt ttaaaattct ttatgtttat ctctataata	70320
ctattgggaa agagagaaag gaaaacctga ctttgttctc atccaaagga ggtgattcca	70380
ctgatttagc caaaataaga cttcctgggt ataataaata ataaagtttt tgatgttttt	70440
tatatggtac ccctactact aggtgatcag acacctctct gcaaaaaaaaa aaaaaatacg	70500
tatgcaataa agttaaagtt ttatgttatt ctttcaaggg gagaaacatc tgtttaacac	70560
agaccagaat atttcaacaa agtcatccca atatttatgg agatcataaa tcaagcgaaa	70620
aaatatattc atcaacaact aaacaaacta cattaaatag tctcaaagca ctttttctact	70680
ttttttctga caggaaaaca ggtttcacaa gtgtgggagac attttaccat ggcttttaac	70740
agtgaggaag gatgttttaa taaagggaag aatttatatg aaagctcaga gaaaagagat	70800
gggtgtggct tgagtgcaca ggtgagagca gatctcatta actgaaatga gagagaagga	70860
aggaattttg caaatatgga aagataacta gtgcaagttt gaacagatta tgtcaatcaa	70920
tgtagaattt ggctatcttt ttaatcaaag aagactatgg aatattttat aggtgtttgc	70980
ttatactcaa agtttttaaag aaataacagt atgaatttgg ttgaactaat ttttttcata	71040
gataggattc tccaagtta tatagcatat atatttctta actagttatt cttcctttta	71100
catatattgt gccacattga gtaacaacta acctgctaag agctattggg ttttaaaaga	71160
taattaatat tagaaagtga tcatttttct gtttcatatt aaacatgata ttctgaaaaa	71220
gcaacattgc ctgaatgttc tacattttat ctttttgaaa acaggtttta taagagattt	71280
cttgtgaaaa gctgaacggt ctgacactga aataagtcag ctaactcaaa gctaagctta	71340
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aaatgtttta acagatttta atccgtagta caagcattat tgatcttaaa ttttaaggata	71460
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ctctatcagg aaaatgtcag gtatccgatg aaaatagata tatgaggtgc caggatatcta	72000
ttccaaactt ggatatcact tcaattagca tcatcttttt ttttttttaa agtgtctaag	72060
gttagaatag tcaccagata ttcccatgta tgaagcaatt ttctgcaaag gccgctgtgg	72120

Corrected Sequence Listing2.ST25

atgatctttt	taaaatatat	attctgggag	acattgagta	aagagaaatt	atttaccaga	72180
gaatgaagaa	ccgaggcccc	attctttggc	tttctgccaa	agatgctgaa	ggcagtgatg	72240
aatgacaaat	acattaccaa	ggaattctcc	ctctaagagg	ctgacaaaga	tctgattttt	72300
aggattatat	taccaccaag	aagatacccc	ttgtcactga	gcttctaata	gaaatatggt	72360
ctatactgaa	acaatttctc	gttctttttc	tttctatctt	tttttgagtt	attttatctt	72420
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gtataataca	tatatattat	ttactttatt	cctgtgttgc	tttggcttgg	tgagactagg	72660
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acttaaatac	aaataatcaa	ttttgcaggc	acaaaatact	tcaaacaaaa	tctgaaatca	72840
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aatgagtggg	gtgatatcct	gctttacttt	gtactggtga	gttctgggtg	ccacctttga	73020
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aaacaaaaaa	ccacctcctt	tacttttagct	gagaaagaag	ttattaggta	cagcttgaca	73140
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caaagggtata	tttagaaatc	atttcatttc	caccaaatat	aataggcatc	tattttattt	73440
attaattaca	gtagaactgc	atttactcag	tgctactgtg	cattattaat	acatactagt	73500
tgtattaata	gttgatttaa	tacatactag	tagtattaat	acatactacg	ttggtattaa	73560
tgtgatcaga	atcctagaat	tttagaacag	tgacttccat	tatcagataa	tttttaaact	73620
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tggagatgga	gtggttggtt	aatacatgca	tatctgactt	caggcaaaac	aaaccatta	73740
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tagataattt	tgaacaata	aaaacaacgg	gtgaaaggta	gctctgtttt	aaattattcc	73920
tatgcttaag	caattctaaa	caatgaaagg	ggtatttctg	ccactgcccc	taccctggg	73980
ttcaccactg	aagaaatgct	cattattaat	atcgtgtcat	ttttttcctt	tacattgggt	74040

Corrected Sequence Listing2.ST25

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tgtagctcct tttccctcca ctccaccaa acaatgctct ccaggatcag cagaaaactta	74280
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agcatttgat gctgatattc atttcttcct atgtgaaaca tccggttttt ctaatgttcg	74400
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ttttattaat gtgctaatag ctaataactg tcaaactctag gtctccaggc caggctctgt	74640
atatccagct accaagagag aactccacgt ggatatcttt ggatgtctgt tttgcatctt	74700
aaacctaact tctccaaatt tgcacttgtc ttctgtctca gacctgctgc tccttcagtg	74760
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ttcttgttct gttgttgcatt tgcataattcc atatttcagc tatcctgaat tgttttcaat	75240
tattcataag ttctttatga attgtgttca ttccatttgg aatattctac cttgtttgat	75300
cagcataaag acttttcgag acactgcagc agcagtgaac ctaaataatgt ttccttgacc	75360
cctacattga atgacacccc ctgtgatatg tttctggaag cagcaatact tcccttctta	75420
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aacaggggtt tatttgaatt tttaaaagaa gaataaagta atttttaaat gaatttcaat	75600
ttaaatttta ggaaaacaat tatataaagt gagatatgct taaattgaag gacaaagtag	75660
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gtgatgcatg gaaaattact gcatatttaa agcttatctt agagctataa taaagcagct	75780
tatgttctaa atcttcatgt cgtaaataagg tccagaaggg atttaaaaag ccttaatcct	75840
tactttaaca cagcacaagt cactgaagtg aaacttgctg aaaggattcc ttttatgtta	75900

Corrected Sequence Listing2.ST25

ggcaacaggt agctgaatat atctacagaa attgaaaaat tggaaattctt ttgctcagaa	75960
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atatgaaaaa ataatttgct aggtttttaa actaacaaaa accatgggta taaaggtttg	76080
aatatatata ggatagttag attgtatttc tgtaatatta aaactcagca ttaaatttaa	76140
tgaacacaaa gtgattctta tcacattgac cattgacatt acatggaaaa aatagtcagt	76200
tggactaatt atgtgtcttt ccatgggta ttaaggtaat tgtatggcat ataaatttat	76260
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ttttaacata tgatcttaa agatatattt ggaatgacac aacagtttta tagacaggcc	76380
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catcacattc attaacaaag ttgataaat gactatagtc tataataaaa ttttttggt	76500
tacaaacata tttaaacacc tgctattaag tataggcatt atcagatctt aaaatacaaa	76560
gatttaaaaa attaccctgt ggtcatggag ctcaaatcc actgcaaaaa taatgtttgt	76620
gataagaaat ttgaaagttg aaggtaatag aaaattttac ctttattttt caaaatgtac	76680
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gaaaataaat tagttccttt atggaactaa tgtaaggaaa atactaagca aacatgta	77280
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caagcactaa aaaagaaatt gttagggaac agtaaaatgc atttccttca tttcacaata	77760
ttattaatat tatggctttg ctaatcttta ttggtgaatg cagtcataat tgaaggtaac	77820

Corrected Sequence Listing2.ST25

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ctttgtgctt	ttctatttgt	gaaagttaat	tattaggaac	gagctagcaa	atgctacttc	78000
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Corrected Sequence Listing2.ST25

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